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version 5.1.6
- 2004 Compugen Ltd.
GenCore (c) 1993
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OM protein - protein search, using sw model

June 16, 2004, 15:21:38; Search time 17 Seconds (without alignments) 891.319 Million cell updates/sec Run on:

US-09-936-845A-15 Title: Perfect score:

291

1545 1 MELAEFWNDLNTFTIYGPNH......PFVKAYIIKSSKKSKKNEN Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## DOTOCAGO

	Description	003574 caenorhabdi	P49191 caenorhabdi	8	mus m	Q9eqc4 mus musculu	P40319 saccharomyc			ETTE I		sacch	P25358 saccharomyc	mus m		archa				pseud	O14681 homo sapien		Q01345 oncorhynchu		arche		Q09226 caenorhabdi	рошо	pomo	Q8d2w8 wiggleswort	Q59647 pseudomonas	ratt	23 mus muscu	P39129 bacillus su
SUMMARIES	ID	YLF4 CAEEL	YYS3 CAEEL	ELO3 HUMAN	ELO3 MOUSE	ELO4 MOUSE	ELO3_YEAST	ELO4_MACFA				ELO1 YEAST	ELO2_YEAST	ELO2_MOUSE	ELO2_HUMAN	YE21_ARCFU	YKQ5_YEAST	TLCA_RICPR	O85F DROME	NORB_PSEST	E124 HUMAN	IP3T HUMAN	NAHB ONCMY	ALG8 HUMAN	Y771_ARCFU	O6N2 HUMAN	ALG6_CAESL	CTR1_HUMAN	FZD9_HUMAN		NORE PSEAE			LPLC_BACSU
	h DB	1			1 1																								11 1			و	4	2
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	% Query Match		9	1.	31.0	r-	ċ	16.9	Ġ	'n.	15.5	4.	4.		m,	9.9	•	6.3	٠					•	•	•	•	•	•	•	•	•	5.8	•
	Score	1545	564	492	479	263.5	262	261	N	239.5	239	220.5	220	219	214	102	σ	97.5	S	96	95	95	93.5	92	91.5	91.5	91.5	91.5	E O	el 60	90,5	06		89.5
	Result No.		N	М	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	53	30	31	32	33

P18794 streptococc P21548 gallus gall	Ogjlg4 mus musculu PS1533 saccharomyc OS2535 Klebsiella	250097 inconsecution P35855 lactobacill P18507 homo sapien	P34322 caenorhabdi Q92e15 rickettsia Q92670 zymomonas m
AMID STRPN GAC2 CHICK	P2L2_MOUSE PDRA_YEAST CAH_KLEPN	E124 MOUSE DLTB LACRH GACZ HUMAN	YKTA_CAEEL Y147_KICPR GNTP_ZYMMO
HH	ललन	ન ભ ભ ભ	Н п п
308 474	621 1564 246	358 405 467	590 236 451
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## ALIGNMENTS

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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=Bristol N2;
MEDIINE=SH50718; DubMed=7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Cracton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jachtning J., Lioyd C., Mortinore B., O'Callaghan M.,
Latreille P., Lightning J., Lioyd C., Mortinore B., O'Callaghan M.,
Parsons J., Saldon N., Smith A., Sounhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Materston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Mohldman P.,
Mohldman P.,
M., Weinston R., Wainston M., Wainstone from chromosome III of C.
                                                                                                                                                                      Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 291;
                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 34.1 kba protein C40H1.4 in chromosome III.
C40H1.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
66572272A53B343F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1545; DB 1;
Pred. No. 4.3e-121;
                                291 AA
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                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wormbep; C40H1.4; CE00112.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
Hypothetical protein; Transmemb:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34059 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z19154; CAA79555.1; -. PIR; S28299; S28299.
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274
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291 AA;
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Best Local Similarity
                                  YLF4 CAREL
Q03574;
01-FEB-1994 (
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RESULT 1
YLF4 CAEEL
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221 TVQTTQMLAGVGITWMVXKVKT--EYKLPCQQSVANLYLAFVLYVTFAILFIQFFVKAYI 278
                                                                                                                                                                                                                                      245 TLQLAQMVMGVIGVTVYRIKSSGBY---CQQTWDNLGLCFGVYFTYFLLFANFFYHAXV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Riausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buctow K.H., Scheafer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buctow K.H., Scheafer C.F., Bhat N.K., Diatchenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L., A Diatchenco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toehhyuki S., Carninci P., Prange C., Brownstein M.J., Nofar T.B., Toehhyuki S., Carninci P., Prange C., Brownstein M.J., Nofar T.B., Toehhyuki S., Carninci P., Mullahy S.J., Bosak S.A., McEwan P.M., McFerran K.J., Malek J.A., Gunaratne P.H., Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Fale S., Garcia A.M., Gabbs R.A., Villalon D.K., Muzny D.M., Sodardia A.M., Gabbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bhakesley R.W., Touchman J.W., Schautz J., Myers R.M., Bulkesley R.W., Touchman J.W., Schautz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Greenertion and initial analysis of more than 15,000 full-length
                       65 SRVITFESSLQNAIKNRNRKSLNSSQMFQIMEKYKPPQLDTPLFVWNSFLAIFSILGFLR 124
                                                                     103 FSIDPLRSLYAEG--FYKTLCYSCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIF 160
QKF--MENRKPFTLKYPLILWNGALAAFSIIATLR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse genomes..;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in a membrane event related to cellular proliferation in brown adipose tissue. Could be implicated in synthesis of very long chain fatty acids and sphingolipids. May catalyze one or both of the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated acyl COA derivative (By similarity)
                                                                                                                                           161 LHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                    099HB03; Q8NHB0;
28-FFB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Blongation of very long chain fatty acids protein 3 (Cold inducible
glycoprotein of 30 kba).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Semina E.V., Murray J.C.;
"The CIG30/PITX3/GBF1 gene configuration is conserved between human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                      270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 35-270 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                          279 IKSSK 283
                                                                                                                                                                                                                                                                                                                               302 KKNNR 306
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BLO3 HU
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                                                                                                                             180
                                                                                                                                                                                                       240
                                                                                                            LYFILIKVIÇKFMENRKPFTLKYPLILMXGALAAFSIIATLRFSIDPLRSLYAEGFYKTL 120
                                                                                                                                                                                                                                                         TAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKV 240
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                                                             1 MELAEFWNDLNTFTIYGPNHTDMTTKYKYSYHFPGEQVADPQYWTILFQKYWYHSITISV
                                                                                                                                                                                                                                                                               TAAGREYILMNYEAHSLMYTYYTVSAMGYRLPRWVSMTVTTVQTTQMLAGVGITWMVYKV
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                                                                                                                                                                                    CYSCNPTDVAAFWSFAFALSKIVBLGDTMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEH
                                      1 NELABPWINDLNTFTIYGPNHTDMTTKYKYSYHPPGEQVADPQYWTILFQKYWYHSITISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWITKY----KYSYHEPGEQVADPQYWTILFQKYWYHSITISVLYFILI----KVI-----
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                               241 KTEYKLPCQQSVANLYLAFVIYVTFALLPIQFFVKAYIIKSSKKSKSVKNE 291
                                                                                                                                                                                                                                                                                                                                                  241 KTEXKLPCQQSVANLYLAFVIYVTFAILFIQPFVKAYIIKSSKKSKSVKNE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
STRAIN=Bristol N2;
Du Z., Gattung S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the ELO family.
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   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1995 (Rel. 33, Last sequence update)
28-FEB-203 (Rel. 41, Last annotation update)
Hypothetical 51.5 kDa protein D2024.3 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
F7940A74A1969914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.5%; Score 564; DB 1;
42.0%; Pred. No. 1.4e-39;
tive 45; Mismatches 86;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             435
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   0;
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InterPro; IPRO02076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51480 MW;
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   291; Conservative
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259
298
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239
278
278
435 AA;
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SEQUENCE
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Best Local 8
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involved in the recruitment of brown adipose tissue.";
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 MLAGVGITWMYYKVKTEYKLPCQOSVANLYLAFVIYYTPAILFIQFFVKAYI---IKSSK 283
210 MFVGAIVSILTYIWRQDQ--GCHTTWEHLFWSFILFMTYFILFAHFFCQTYIRPKVKAKT 267
                                                                                                                                                                                                                                                                                                                                    POKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                                                                                                              108 LRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH 166
                                                                                                                                                                                                                                                                                                                                                                                         90 GEVLITGGLKQTVCFINFIDNSTVKFWS#VFLLSKVIBLGDTAFIILRKRPLIFIHWYHH 149
                                                                                                                                                                                                                                                                                                                                                                                                                       AAVIIYTVHSGAEHTAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                    30 FEEYWATSFPIALIYLVLIAVGQNYMKERKGFNLQGPLILWSFCLAIFSILGAVRMWGIM 89
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Elongation of very long chain fatty acids protein 3 (Cold inducible glycoprotein of 30 kDa) (CIN-2)
                                                                                                                                                                                                                                                 ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Cig30, a mouse member of a novel membrane protein gene family, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                          9
                                                                                                                                                                              Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum. RRANSMEM 29 49 POTENTIAL.
                                                                                                                                                                                                                                                                                          Score 492; DB 1; Length 270;
Pred. No. 7.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6; TISSUE-Brown adipose tissue;
MEDLINE-98058971; PubMed=9395518;
Tvrdik P., Asadi A., Kozak L.P., Nedergaard J., Cannon B.,
                                                                                                                                                                                                                                                                                                                 87; Indels
                                                                                                                                                                                                                                                            (POTENTIAL).
OCGCBF1E7B5DE8B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AA.
                                                                                                                                                                                                                                                                                                                 53; Mismatches
            SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                        Genew, HGNC:18047; ELOVL3.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
                                                                                                                  EMBL; BC034344; AAH34344.1; -.
EMBL; AF292387; AAG17875.1; -.
                                                                                                                                                                                                                                                                      31500 MW;
                                                                                                                                                                                                                                                                                           31.8%;
39.9%;
  reticulum (Potential).
                                                                                                                                                                        PROSITE, PS01188, ELO, 1.
                                                                                                                                                                                                                                                                                                                 97; Conservative
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                                                                                                                                                                                              49
86
186
218
255
268
                                                                                                                                                                                                                                                                     270 AA;
                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 KSK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSQ 270
                                                                                                                                                                                                        66
164
198
235
266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELO3 MOUSE
                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                      48
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                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- INDUCTION: Elevated in brown adipose tissue in conditions of brown fat recruitment, namely cold stress, perinatal development and after diet-induced thermogenesis. A symergistic action of both catecholamines and glucocorticoids is required for the induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Readily detected in brown adipose tissue and liver. Weak expression in Kidney, white adipose tissue, heart and skin. Not detected in lung, testis, muscle, spleen, brain, thymus and intestine.
                                                                  STRAIN=129/SvJ;
MEDLINE=99403085, PubMed=10473596;
MEDLINE=99403085, PubMed=10473596;
MEDLINE=99403085, PubMed=10473596;
Nedergaard J., Jacobsson A.;
Cig3o and Pitx3 genee are arranged in a partially overlapping arial-to-tail array resulting in complementary transcripts.";
J. Biol. Chem. 274:26387-26392(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
Biol. Chem. 272;31738-31746(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1195976; Elov13.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PP01151; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF054504; AAD51088.1; -. BC016468; AAH16468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U97107; AAC06127.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reticulum (Potential)
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                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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or send an email to license@isb-sib.ch)
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                                                                                         62
98
185
208
310
                                                                                                                                                                       20
312 AA;
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [3]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P40319;
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ELO3_YEAST
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                                                                                                                4
                                                                                                                                                                                                                               AVLIYTVHSGABHTAAGRFYILMNYFAHSIMYTYYTVSAMGYRLPKWVSMTVTTVQTTQM 227
                                                                                                                                                                                                                                                                                      QKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL 108
                                                                                                                                                                                  109 RSLYABGGTYKTLCYSCNPTD-VAAFWSPAPALSKIVBLGDTWFIILRKRPLIFLHYYHHA 167
                                                                                                                                                                                              TVILETSFCYKNKVPSGGWFWTWNFGVHSVMYTYTWKAARLAGFULPWVITSLQILQM 211
                                                                                                                                                                                                                                                                            LAGV--GITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSK-K 284
                                                                                                                                                            5
                                                                                                                                                     reticulum (Potential).
TISSUB SPECIFICITY: Expressed in the adult retina, exclusively in
photoreceptor cells.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CSTBE,/6; TISSUE=Testis;
MEDLINE=20578755; PubMed=11138005;
MEDLINE=20578755; PubMed=11138005;
MEDLINE=20578755; PubMed=11138005;
Metzker M.L., Allikmets R., Zack D.J., Kakuk L.B., Lagali P.S.,
Wong P.W., McDonald I.M., Sieving P.A., Figueroa D.J., Austin C.P.,
Gould R.J., Ayyagari R., Petrukhin K.;
M.A. S.-bp deletion in ELOVIA is associated with two related forms of
autosomal dominant macular dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genet. 27:89-93(2001).
FUNCTION: Involved in the biosynthesis of very long chain fatty acids. Seems to represent a photoreceptor-specific component of the fatty acid elongation system residing on the endoplasmic
            POTENTIAL.
POTENTIAL.
ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                       N-LINKED (GLCNAC. . .) (POTENTIAL) P7CA96199BE89401 CRC64;
                                                                                                                8
                                                                                         Length 271;
                                                                                                                87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 28-FBB-2003 (Rel. 41, Created)
26-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Blongation of very long chain fatty acids protein
BLOVL4.
                                                                                         Score 479; DB 1;
Pred. No. 9.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                      Ą
                                                                                                                47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                     312
                                              (POTENTIAL)
  POTENTIAL
                                                          6 N
32060 MW;
                                                                                         31.0%;
                                                                                                    Matches 101; Conservative 4
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  187
219
256
269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                  271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                              270
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                                                                                                                                                                                                                                                                                                   212
            TRANSMEM
TRANSMEM
SITE
                                                       CARBOHYD
SEQUENCE
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                                                                                          Query Match
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  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AFWSFAFALSKIVELGDTMFIILRKR--PLIFLHYYHHAAVLIYTV-HSGAEHTAAGR-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 FYILMOYFAHSLMYTYYTVSAMGYRLPK--WVSMTVTTVQTTQMLAGVGITWMVYKVKTB 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 KYPLILMNGALAAPSIIATLRFSIDPLRSLYAEGFYKTLCYSCNPTD------VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 DMITKYKYSYHPPGBQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTL
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POTENTIAL.
ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation of fatty acids protein 3 (SUR4 protein) (SRE1 protein)
(v-SYARE bypass mutant gene 1 protein).
ELO3 OR SUR4 OR SRE1 OR APA1 OR VBM1 OR YLR372W OR L8039.2.
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MEDLINE=96220455; FubMed=8649379;
MEDLINE=96220455; PubMed=8649379;
Silve S., LepLatois P., Josse A., Dupuy P.-H., Lanau C., Kaghad Silve S., LepLatois P., Josse A., Taton M., Le Fur G., Caput D., Dhers C., Picard C., Rahler A., Taton M., Le Fur G., Caput D.,
                                                                                                                                                                                                                                                                                                                                                                          .) (POTENTIAL). CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CPFP----KWMHWALIAYAISFIFLFINFYTRITNEPKQSKTGKTATN 284
                                                                                                                                               Transmembrane; Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrara P., Loison G., "The immunosuppressant SR 31747 blocks cell proliferation by inhibiting a steroid isomerase in Saccharomyces cerevisiae.", Mol. Cell. Biol. 16:2719-2727(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1, Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 YKLPCQQSVANLYLAFVIY-VTFAILFIQFFVKAY-IIKSSKKSKSVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 263.5; DB 1; Length 28.7%; Pred. No. 7.8e-15; ive 53; Mismatches 108; Indels
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Bukaryota, Pungi, Ascomycota, Saccharomycotina; Sacch
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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B04CD48024772132 (
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Thesis (1994), University of Bordeaux II,
                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
EMBL: AF277093; AAG47667.1; -. MGD; MGI:1933313; Elov14.
InterPro; IPR002076; GMSI_SUR4.
PROSITE; PS01181; ELO; 1.
PROSITE; PS01188; ELO; 1.
PROSITE; PS01188; ELO; 1.
TRANSMEM 42 62 POTE
TRANSMEM 78 98 POTE
TRANSMEM 165 185 POTE
TRANSMEM 188 208 POTE
TRANSMEM 246 266 POTE
TRANSMEM 246 266 POTE
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36520 MW;
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STRAIN=ATCC 44827 / SKQ2N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83; Conservative
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MAINTENESTRANCE 91222924; MARGERAGE NOTO G a new gene involved in this grants. Marked. MAINTENESTRANCE 9122924; MAINTENESTRANCE 9123924; MAINTENESTRANCE 9123925; MAINTENESTRANCE 9123924; MAINTENESTRANCE 9123925; MAINTENESTRANCE 91239239; MAINTENESTRANCE 9123925; MAINTENE
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50 FEYFSGYPAEQFEFIHNKTFLAN--GYHAVSIIIVYYIIIFGGQAILKALNASPLKFKLL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 VELGDIMPIILRKRPLIFIHYYHH--AAVLIYTVHSGAEHTAAGRPYILMNYFAHSLMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 VELIDTVFLVLRRKKLLFLHTYHGATALLCYTQLIG--RTSVEWVVILLNIGVHVIMYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 LILWNGALAAPSIIATLRPSIDPLRSLYAEGPYKTLC--YSCNPTDVAAFWSFAPALSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBY-----KLPCQ
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TISSUE SPECIFICITY: Expressed mainly in retina. Also expressed in
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-:- FUNCTION: Involved in the biosynthesis of very long chain fatty acids. Seems to represent a photoreceptor-specific component of the fatty acid elongation system residing on the endoplasmic the fatty acid elongation system residing on the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metacas, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
Cercopithecinae, Macaca
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MEDLINE=22691545; PubMed=12806887;
Umeda S., Ayyagari R., Suzuki M.T., Ono F., Iwata F., Fujiki K.,
Kanai A., Takada Y., Yoshikawa Y., Tanaka Y., Iwata T.;
"Molecular cloning of EL/OVL4 gene from cynomolgus monkey (Macaca fascicularis)";
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., 7
Suzuki Y., Sugano S., Hashimoto K.;
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                      Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.0%; Score 262; DB 1; Length 34
28.9%; Pred. No. 1.2e-14;
ive 53; Mismatches 115; Indels
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1303A9ACS4BFFCCS CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Blongation of very long chain fatty acids 4 protein.
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W -> R (IN REF. 3).
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es 82; Conservative
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345 AA;
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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishil S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Nabo human cDna sequencing project.";
"NEDO human cDna sequencing project.";
"Nebo human cDna sequencing project.";
                                                                                                                                  MEDLINE=21464738; PubMed=11581213; Edwards A.O., Donoso L.A., Ritter R. III; Edwards A.O., Donoso L.A., Ritter R. III; Anovel gene for autosomal dominant Stargardt-like macular dystrophy with homology to the SIMA protein family."; Invest. Ophthalmol. Vis. Sci. 42:2652-2663(2001).
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MEDLINE=20578755; PubMed=11138005;
                                                                                             Nat. Genet. 27:89-93(2001).
                                                                                                                          SEQUENCE PROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RWBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 KYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGF---YKTLC----YSCNPTDV----A 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AFWSFAFALSKIVELGDTMFILLRKR--PLIFLHYYHHAAVLIYTV-HSGAEHTAAGR-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 FYILMNYFAHSLMYTYYTVSAMGYRLPK--WVSMTVTTVQTTQMLAGVGITWMVYKVKTE
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                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
560FE00C91D96766 CRC64;
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Fatty acid biosynthesis; Transmembrane, Endoplasmic reticulum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.9%; Score 261; DB 1; Length 314; 30.3%; Pred. No. 1.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97; Indels
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                SIMILARITY: Belongs to the BLO family.
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                                                                                                                                                   EMBL, AF461182, AA015594.1, --
EMBL, AF461187, AA015601.1, --
EMBL, AF461184, AA015601.1, JOINED.
EMBL, AF461184, AA015601.1, JOINED.
EMBL, AF461185, AA015601.1, JOINED.
EMBL, AF461185, AA015601.1, JOINED.
EMBL, AB063100, BAB60806.1, --
InterPro, IPR002076; GMS1_SUR4,
Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
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36812 MW;
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314 AA;
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MEDLINE=22480060; PubMed=1259226;
Rivolta C., Ayyagari R., Sleving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sleving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sleving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sleving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sleving P.A., Berson E.L., Dryja T.P.;
Tetinitis pigmentosa and Leber congenital amaurosia.",
Mol. Vision 9:49-51(2003).
I. FUNCTION: Involved in the biosynthesis of very long chain fatty acid elongation system residing on the endoplasmic the fatty acid elongation system residing on the endoplasmic reticulum. May be implicated in docosabaxaenoic acid (DHA) biosynthesis, which requires dietary consumption of the essential alpha-linolemic acid and a subsequent series of three elongation steps.
C.-- SUBCELULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential).
C.-- TISSUE SPECIFICITY: Expressed in the retina and at much lower
NEUGREPATES STATES TO STATE STATES ST
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606;

SEQUENCE FROM N.A., AND VARIANT VAL-299. TISSUE-Retina;

ELO4 HUMAN STANDARD; PRT; 314 AA. Q9GZR5; Q86ZR5; Q86ZR1; Q9H139; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 11-OCT-2003 (Rel. 43, Last annotation update) 11-OCT-2003 (Rel. 4

HUMAN

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Mus musculus (Mouse).
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level in the brain.

DISBABS: Defects in ELOVL4 are the cause of Stargardt disease 3 (STGD3) [MIM:500110]. STGD3 is an autosomal dominant form of macular degeneration characterized by decreased visual acuity, macular atrophy, and extensive fundus flecks.

DEFAGE: Defects in ELOVL4 are a cause of autosomal dominant Stargardt-like macular dystrophy (ADMD) [MIM:500110].

SIMILARITY: Belongs to the ELO family.

DATABASE: NAME-MUtations of the ELOVL4 gene;

NOTE-Retina International's Scientific Newsletter;

WWW="http://www.retina-international.com/sci-news/elovlmut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Mismatches 105; Indels
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Q -> R (IN REF. 4).
B2BBCE54D868E96E CRC64;
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FFIEd=VAR_017043.
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PROSITE; PS01188; ELO; 1.
Fatty acid biosynthesis; Transmembrane; Polymorphism; Stargardt disease; Vision 20 Polymorphism; Stargardt disease; Vision 20 Polymorphism; Polymorphism; Stargardt disease; Polymorphism; Stargardt disease; Vision 20 Polymorphism; Vision 20 Pol
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314 AA;
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MIM; 600110;
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                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Expressed in a broad variety of tissues. Highly expressed in scomedh, lung, kidney, skin and inteefrine. Moderately expressed in white adipose tissue, liver, spleen, brain, brown adipose tissue, heart and muscle. Weakly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIMPILLRKR--PLIFLHYYHHAAVLIYTVHSGAEHT--AAGRFYILMNYPAHSLMYTYY
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Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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POTENTIAL.
ENDOPLASMIC RETICULUM RETRIBVAL MOTIF
                                                                                               Nature 409:685-690(2001).

-!- FUNCTION: Could be implicated in tissue-specific synthesis of long chain fatty acids and sphingolipids. May catalyze one or of the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated acyl CoA
                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                    derivative.
SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
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TRANSMEM 23 43 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the ELO family.
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InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF170907; AAF72572.1; -. EMBL; BC006735; AAH06735.1; -. EMBL; AK003743; BAB22975.1; -.
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nes 78; Conserv
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PROSITE;
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A KLUSUE-KIGHOPY;

A KLUSUE-LAIGHOPY;

A KLUSTER FD., Collins F.S., Wagner L., Shemen C.R., Schuler G.D.,

A Altschul S.F., Zeeberg B.B., Butchew K.H., Schaefer C.F., Bhat W.K.,

A Altschul S.F., Zeeberg B.B., Butchew K.H., Schaefer C.F., Bhat W.K.,

A Altschul S.F., Zeeberg B.B., Butchew K.H., Schaefer C.F., Bhat W.K.,

BA Altschul S.F., Zeeberg B.C., Max S.I., Wang J., Hsieh F.,

B Datchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Hillalon D.K., Muzry D.M., Sodergen B.J., Lu X., Gibbs R.A.,

R Hakesley R.W., Tuckman J.W., Sodergen B.J., Lu X., Gibbs R.A.,

R Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.,

R Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.,

R Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length

RT Proc. Natl. Academces.

C - PUNCTION: Could be implicated in tissue-specific synthesis of very long chain fatty acids and sphingolipids. May catalyze one or both corversion of beta-ketoacti Corversion of beta-ketoacti C.C.

Reduction of beta-ketoacti C.A. to beta-hydroxyacyl CoA or reduction of tear ketoacti C.C.

Reduction of beta-ketoacti C.C.

R C.C. Reduction of tear setoaction in fatty acid acid acid acid and sphingolipids. Acid acid.

R C.C. Reduction of beta-ketoacti C.C.

R C.C. Reduction of beta-hydroxyacyl CoA or reduction of beta-hydroxyacyl CoA or reduction of tear setoaction in fatty acids and spingolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.

ISOGAI T., Ote T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,

Matsurawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

Nakamura Y., Nagahari K., Masuho Y., Saeaki N.;

"NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

derivative (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential).
-!- SIMILARITY: Belongs to the ELO family.
-!- CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 189.

                                                                                                                                                                                                    Buteleostomi;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=20272150; PubMed=10810093; Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C., Indication of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.", Genome Res. 10:703-713(2000).
                   OSBWGO: OSNVD9; Q9Y396;
28-FEB-2003 (Rel. 41, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
Slongation of very long chain fatty acids protein 1 (CGI-88)
ELOVU1 OR SSC1.
                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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EMBL; AK001653; BAA91813.1; -.
EMBL; BC000618; AAH00618.1; -.
                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                              74 LYIVYEFLM-----SGWLSTYTWRCDEVDYSNSPEALRMVRVAWLFLF--SKFIELM 123
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                                                                                                                                                                                                                                                                                                                                                                    203 TVSAMGYRLP-----KWVSMTVTTVQTTQ-MLAGVGITWMVYKVKTBYKLPCQQSVANLY 256
                                                                                                                                                                                                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                                                                      DTMFIILRKR--PLIFLHYYHHAAVLIYTVHSGAEHT--AAGRFYILMNYFAHSLMYTYY 202
                                                                                                                                                                                                                           96
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                                                                                                                                                                                                                                        IIATLRFSIDPLRSLYAEGFYKTLCYSCNPTD------VAAFWSFAFALSKIVELG
                                                                                                                                                                                                                                                                                                                                   183 GLSAPG---PVAQPYLWWKKHMTAIQLIQFVLVSLHISQYYFMSSCNYQYP----VIIH
                                                                                                                                                                                                                           39 ADP--QYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILMNGALAAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE 95274326; PubMed=7754713; Purnalle B., Coster F., Goffeau A.).

Purnalle B., Coster F., Goffeau A.).

The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies 24 open reading frames including NUC1, PRP21 (SPP91), CDC6, CRY2, the gene for 824, a homologue to the aconitase gene AC01 and two homologues to chromosome III genes.";

Yeast 10:1235-1249(1994).

-!- FUNCTION: May be a membrane bound enzyme involved in the highly specific elongation of saturated 14-carbon fatty acids (14:0) to 16-carbon species (16:0).
                                                                                                                 ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
(POTENTIAL).
S -> P (IN REF, 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=96324909; PubMed=8702485;
Toke D.A., Martin C.E.;
"Isolation and characterization of a gene affecting fatty acid elongation in Saccharomyces cerevisiae.";
J. Biol. Chem. 271:18413-18422(1996).
                                         Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
TRANSMEM 23 43 POTENTIAL.
TRANSMEM 61 81 POTENTIAL.
TRANSMEM 176 196 POTENTIAL.
TRANSMEM 201 221 POTENTIAL.
TRANSMEM 231 251 POTENTIAL.
                                                                                                                                                                           15.5%; Score 239; DB 1; Length 279; 28.7%; Pred. No. 7.5e-13; tive 47; Mismatches 97; Indels
                                                                                                                                                     B168EE4C7EAF92A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elongation of fatty acids protein 1.
ELO1 OR YUL196C OR J0343.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                  277
                                                                                                                                                                                                                                                                                                                                                                                                                                         235 LIWMYGTIFFMLFSNFWYHSY 255
Genew; HGNC:14418; ELOVL1.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  LAFVIYVTFAILFIQFFVKAY
                                                                                                                                          68 68 S
279 AA; 32663 MW;
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                       Local Similarity
nes 75; Conserv
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                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
BLO1_YEAST
ID _ELO1_YEA
AC P39540;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 VYK--VKTEYKLPCQQ-----SVANLYLAFVIYVTFAILFIQFFVKAYIIKS-SKKSK 286
SUBCELLULAR LOCATION: Integral membrane protein (Potential). INDUCTION: Induced in wild type cells supplemented with 14:0 fatty acids and repressed when cells are supplied with 16- and 18-carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : : : | | : : : | | : : | | : : | | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LYFILIKVIQKFMENRKPFTLKYPLILMNGALAAFSIIATLRFSIDPLRSLYAEGFYKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X77688; CAA54764.1; -.
EMBL; Z4541; CAA89491.1; -.
EMBL; Z4541; CAA89491.1; -.
EMBL; S46638; S46638.
GermOnline; 141808; -.
SGD; S0003732; ELOI,
GO; GO:0019368; P:fatty acid elongase activity; IMP.
GO; GO:0019368; P:fatty acid elongation, unsaturated fatty acid; IMP.
INTERPO; IRFO02076; GNS1_SUR4.
PROSITE; PS01188; ELO; 1.
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P25358;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation of fatty acids protein 2 (GNS1 protein) (v-SNARE bypass mutant gene 2 protein).
ELOZ OR FENI OR GNS1 OR VEM2 OR YCR034W OR YCR34W OR YCR521.
Saccharomycos cerevisiae (Baker's yeast).
Saccharomycos scerevisiae (Baker's yeast).
Saccharomycotals. Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetese;
NUEL_TAXID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                                                                                               SIMILARITY: Belongs to the ELO family.
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121
207
255
292
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272
310 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99054745; PubMed=9832547;
David D., Sundarababu S., Gerst J.E.;
Involvement of long chain fatty acid elongation in the trafficking of secretory vesicles in yeast.";
J. Cell Biol. 143:1167-1182(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. Biol. Chem. 272:17376-17384(1997).

-!- FUNCTION: Involved in synthesis of 1,3-beta-glucan. Could be a subunit of 1,3-beta-glucan synthase. Could be also a component of the membrane bound fatty acid elongation systems that produce the 26-carbon very long chain fatty acids that are precursors for ceramide and sphingolipids. Appears to be involved in the elongation of fatty acids up to 24 carbons. Appears to have the highest affinity for substrates with chain length less than 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION. MEDIMEd=9211877;
MEDIME-975220; PubMed=9211877;
OD C.-S., Toke D.A., Mandala S., Martin C.E.;
*ELOZ and ELO3, homologues of the Saccharomyces cerevisiae ELO1 gene, function in fatty acid elongation and are required for sphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
MEDLINE=95286506; PubMed=7768822;
El-Sherbelini M., Clemas J.A.;
"Cloning and characterization of GNS1: a Saccharomyces cerevisiae gene involved in synthesis of 1.3-beta-glucan in vitro.";
J. Bacteriol. 177:3227-3234(1995).
                                                                                                                                                                                                                      MEDINE=92133166; PubMed=1776366; Wicksteed B.L., Roberts A.B., Sagliocco F.A., Brown A.J.P.; Wicksteed B.L., Roberts A.B., Sagliocco F.A., Brown B.J.P.; arthe complete sequence of a 7.5 kb region of chromosome III from Saccharomyces cerevisiae that lies between CRYI and MAI.";
             MEDLINE=91181345; PubMed=1264349;
Thierry A., Fairhead C., Dujon B.;
"The complete sequence of the 8.2 kb segment left of MAT on chromosome III reveals five ORFs; including a gene for a yeast ribokinase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0009922; F:fatty acid elongase activity; IMP.
GO; GO:0030497; P:fatty acid elongation; IMP.
GO; GO:0030148; P:sphingolipid biosynthesis; IMP.
GO; GO:0030148; P:sphingolipid biosynthesis; IMP.
InterPro; IPR002076; GNS1_SUR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ELO family.
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PROSITE, PS01189; E.O.; 1.
Patty acid biosynthesis; Transmembrane.
TRANSMEM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X56909; CAA40226.1; -.
EMBL; X59720; CAA42301.1; -.
EMBL; AF012655; AAB87766.1; -.
PIR; S12916; S12916.
GermOnline; 138940; -.
SGD; S0000630; FEN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S78624; AAB21260.1; -.
                                                                                                                                                    Yeast 6:521-534(1990).
                                                                                                                                                                                                                                                                                                                         Keast 7:761-772(1991)
                                                                                                                                                                                                 SEQUENCE FROM N.A.
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XX MEDLINE=2108566; PubMed=11217851;
XX MEDLINE=2108566; PubMed=11217851;
XX MEDLINE=2108566; PubMed=11217851;
XX MEDLINE=2108566; PubMed=11217851;
XX Arakawa T., Shinaqawa A., Shibata K., Yoonno H., Adachi J., Fukuda S., Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Astawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Gasvant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Gasvant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Kochiwa H., Kadota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M., Bult C., Fletcher C., Fulita M., Gariboldi M., Bult C., Romstein M.J., Machionni I., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Rosaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Nimhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Namachi V., Namachi V., Namachi V., Kawaji H., Kohtsuki S., Namachi V., Namachi V., Kawai V., Kawaji H., Kohtsuki S., Namachi V., Namachi V., Kawai V., Kawaji H., Kohtsuki S., Namachi V., Namachi V., Kawai V., Kawaji H., Kohtsuki S., Namachi V., Kawai V., Kawaji H., Kohtsuki S., Namachi V., Namachi V., Kawai V., Kawaji H., Kohtsuki S., Namachi V., Kawai V.
                                                                                                                                                                                                                                                                                                                                                                                                     62 YFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYABGFYKTLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 YYVIIFGGRFLSKSKPFKLNGLFQLHNLVLTSLSLTLLLLMVEQLVPIIVQHGLYPAIC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 YSCNPTDVAAFWSFAPALSKIVELGDTWFIILRKRPLIFILHYYHH--AAVLIYTVHSGAE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 NIGAWTOPLVTLYYMNYIVKFIEFIDTFFLVLKHKKLTFLHTYHHGATALLCYTOLMST- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 HTAAGREYILMNYRAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVG-ITWMVY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 KVKTEYKLP-----CQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=Liver;
WEDLINE=20253178; PubMed=10791983;
TVICAIR P., Westerberg R., Silve S., Asadi A., Jakobsson A., Cannon B.,
Loison G., Jacobsson A.;
"Role of a new mammalian gene family in the biosynthesis of very long chain fatty acids and sphingolipids.";
J. Cell Biol. 149:707-718(2000).
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                         Length 347;
                                                                                                                                                                                                                                     14.2%; Score 220; DB 1; Length 34
28.2%; Pred. No. 3.5e-11;
ive 36; Mismatches 121; Indels
                                                                                                                                                               24225E49A43A1003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELOZ MOUSE STANDARD; PRT; 292 AA.
COJLJ4; Q9D5Z2;
28-PEB-2003 (Rel. 41, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Rlongation of very long chain fatty acids protein 2.
ELOVL2 OR SSC...
                                           POTENTIAL.
                                                                                                                                                                    40002 MW;
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                                                                                                                                                                                                                                                                                                                               67; Conservative
        221
265
296
341
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                                      245
276
333
347 AA;
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TRANSMEM
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SEQUENCE
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Best Local
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ELO2 MOUSE
                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 VLYFILIKVIQKFMENRKPFTLKYPLILWNGA---LAAFSIIATURFSIDPLRSLYAEGF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 YKTLCY---SCNPTDV---AAFWSPAFALSKIVELGDTMFIILRKR--PLIFLHYYHHAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNLOCONLDSAGEGDVRVAKVLWWYYP--SKLVEFLDTIFFVLRKKTNOITFLHVYHHAS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V-----LIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPK-----WVSM 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 MFNIWWCVLNWIPCGOSF----FGPTLNSFIHILMYSYYGLSV----FPSMHKYLWWKK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 TVITVQITQMLAGVGITWAVYKVKTEYKLPÇQQSVANLYLAFVIYVTFALLFIQFFVKAY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELABEWNDLNTF--TIYGPNHTDMTTKYKYSYHFPGEQVADPQYWTILFQKYWYHSITIS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                              .; IDA.
                                                                                        reticulum (Potential):
TISSUE SPECIFICITY: Highly expressed in testis, lower level in liver. Weakly expressed in white adipose tissue, brain and kidney. SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
FUNCTION: Could be implicated in tissue-specific synthesis of long chain fatty acids and sphingolipids. May catalyze one or to f the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated acyl CoA
                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
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                                                                                                                                                                                                                                                                                                                                                                           biosynthesis, Transmembrane, Endoplasmic reticulum 30 POTENTIAL.
                                                                                                                                                                                                                                                          EMBL; AF170908; AAF72573.1; -.
EMBL; AX014803; BAB29559.1; ALT_INIT.
MGD; MG1.1858960; BLOV12.
GC); GC:0005792; C:microsome; IDA.
GC); GC:0016747; F:transferase activity, transferring groups of GC); GC:0000038; P:very-long-chain fatty acid metabolism; IDA.
InterPro; IPR020205; GNS1_SUR4.
PROSITE; PS01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLKAFDNEVNAFLDNMFGPRDSRVRGWFLLDSYLP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E1959B8DFC43A7D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 219; DB 1;
Pred. No. 3.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 AA; 34207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 IIKSSKK---SKSVKN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 RKKPVKKELQEKEVKN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.2%;
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FRANSMEM
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ID ELO2 HUMAN
AC Q9NXB9;
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28-FEB-2003 (Rel. 41, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 LQCQDLTSAGEADIRVAKVLMWYYP--SKSVEFLDTIFFVLRKKTSQITFLHVYHHASMF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPK-----WVSMTV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 ITVOTTOMLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFALLFIQFFVKAXII 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
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                                                                                                                                                                                                                                                                                                                                  Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Could be implicated in tissue-specific synthesis of very long chain fatty acids and sphingolipids. May catalyze one or both of the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated acyl CoA
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POTENTIAL.
POTENTIAL.
POTENTIAL.
ENDOPLIAL RETICULUM RETRIEVAL MOTIF
(POTENTIAL).
6FB735C4FBEC9FC1 CRC64;
                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derivative (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum. TRANSMEM 32
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation of very long chain fatty acids protein 2.
ELOVIZ OS SSC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK000341; BAA91096.1; -. Genew; HGNC:14416; ELOVL2.
InterPro; IPR022076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
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                                                                                                                                          Homo sapiens (Human).
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Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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260 KPMKKDMQEPPAGKEVKN 277

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                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=VC-16 / DSM 4304 / ATCC 49558;

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlarage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G. (3il S.,

Fleischmann R.D., Quackenbush A., McKenney K., Adams M.D., Loftus B.,

Fleischmann R.D., Dougherty B.-M., McKenney K., Adams M.D., Loftus B.,

Feterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overboek R., Goazyne J.D., Neidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.6%; Score 102; DB 1; Length 880;
ilarity 19.3%; Pred. No. 0.58;
Conservative 47; Mismatches 83; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the UPF0182 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n; Transmembrane; Complete protecue.
41
POTENTIAL.
93 POTENTIAL.
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229 POTENTIAL.
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                                                                                                                                                                                                                                                             Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCbl_TaxID=2234;
                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0182 protein AF1421.
                                                             880 AA
                                                             PRT;
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InterPro; IPR005372; UPF0182.
Pfam; PP03699; UPF0182; 1.
Hypothetical protein; Transmemb)
TRANSMEM 61 93 POTTRANSMEM 103 125 POTTRANSMEM 109 103 125 POTTRANSMEM 109 109 125 POTTRANSMEM 109 125 POT
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                                                             STANDARD;
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152
195
237
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880 AA;
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hes 58; Conserv
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                                                          YE21 ARCFU
028851;
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Matches
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47 LFQXXWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSID 106

107 PLR-------SLYAEGFYKTLCYSCNPTDV------AAFWSFAFALSKIV 143 

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248
144 BLGDTWPIILRKRPLI------YHHAAVLI 171
                          154 -IGSLLAALLISLAIAAFAYMYAFRWVKSLEEFKEIFPGSGFWHFSALLFASFLLSAALI 212
                                                                                                                    285
                                                                                                                                     226 OMLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKS
                                                           172 Y----TVHSGABH-TAAGRPYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTT
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Search completed: June 16, 2004, 15:28:01 Job time : 18 secs

- protein search, using sw model OM protein June 16, 2004, 15:21:03 ; Search time 60 Seconds (without alignments) 1370.355 Million cell updates/sec Run on:

US-09-936-845A-15 1545 1 MELAEFWNDLNTFTIYGPNH......FFVKAYIIKSSKKSKSVKNE 291 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\* Database :

genescq11980s:\* genescq11990s:\* genescq12000s:\* genescq12001s:\* genescq12001as:\* genescq12001as:\* genescq12001as:\*

geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aab00198 Putative	Aab00199 Putative	Aab00205 Putative	Aae04173 Human gen	Abg92079 Human rec	Human	Abb78813 Human NOV		Human	Human			Aau87829 Fruitfly		Aae37330 Human VLC	Aae04172 Human gen	Aay79260 Putative	Aab48959 Mouse fat	Abp56420 Human elo	Aay79249 Human put	Aab00209 Murine se	Aay79264 Putative	Abp56419 Human elo	Abb82959 Human LCE	Abb78814 GNS1/SUR4
	. QI	AAB00198	AAB00199	AAB00205	AAE04173	ABG92079	AAE24550	ABB78813	ABB78812	ABP56418	ABB82960	ABB82966	AAY79263	AAU87829	ABB60310	AAE37330	AAE04172	AAY79260	AAB48959	ABP56420	AAY79249	AAB00209	AAY79264	ABP56419	ABB82959	ABB78814
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₩	Query Match	100.0	36.5	35.4	•	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.4	31.4	31.4	31.3	31.3	31.0	31.0	31.0	31.0	30.9	30.8	30.4	30.4	29.5
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AAE24555	AAY79266	AA329648	AAU00476	AAU87832	AAG79838	AB032607	AB032621	ABB82962	ABB82961	AB007183	AAM93344	AAE04100	ABG64366	AAE04123	ABG64365	ABO32609	AAB00200	AAB00202	AAB86466
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56	27	28	53	30	31	32	33	34	35	36	37	38	e e	40	41	4	43	44	4.5

## ALIGNMENTS

Blongase; polyunsaturated fatty acid; PUFA; dietary supplement; pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid; arachidonic acid; eicosapentanoic acid; docosatrienoic acid; docosatetraenoic acid; docosatetraenoic acid; Putative polyunsaturate fatty acid elongase (PUFA). AAB00198 standard; protein; 291 AA (first entry) 08-FBB-2001 AAB00198; RESULT 1 AAB00198 

Caenorhabditis elegans.

WO200055330-A1

21-SEP-2000.

20-MAR-2000; 2000WO-GB001035.

18-MAR-1999; 99GB-00006307. 18-FBB-2000; 2000GB-00003869.

(UYBR-) UNIV BRISTOL.

Napier JA;

WPI; 2000-647074/62.

Novel isolated polypeptide comprising functional long chain polymnsaturated fatty acid (PUPA) elongase of Caenorhabditis elegans used to produce PUPA for foodstuff, dietary supplement or pharmaceutical composition.

Disclosure; Page 25; 42pp; English.

New elongase polypeptides which are functional long chain polyunsaturated fatty acid (PUFA) elongase polypeptides are described. The elongase catalyses an elongase reaction to produce PUFA (24 carbon fatty acid with at least 4 double bonds) such as di-homo-gamma-linoleic acid (20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14), elocaspentanoic acid (20:5Delta5,8,11,14), docosatentanoic acid (20:5Delta5,8,11,14), docosatentanoic acid (22:3Delta7,10,13,16), docosapenteanoic acid (22:5Delta7,10,13,16,19) or docosabexaenoic acid (22:5Delta7,10,13,16,19) or docosabexaenoic acid (22:6Delta7,10,13,16,19) or docosabexaenoic acid

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                                                                                                                                                                                                                               KTEYKL, PCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSKVKNE
                                              Length 291;
                                                               Indels
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                                             100.0%; Score 1545; DB 3;
100.0%; Pred. No. 2.7e-161;
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dietary supplements and in pharmaceutical used to elavate PUFA levels of an animal o
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                                                        Similarity
                             Sequence 291 AA;
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(20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14), eicosapentanoic acid (20:5Delta5,8,11,14,17), docosatrienoic acid (22:3Delta3,16,19), docosatetraenoic acid (22:4Delta7,10,13,16), docosabexaenoic acid (22:5Delta4,7,10,13,16,19) or docosabexaenoic acid (22:5Delta4,7,10,13,16,19). FUFA produced is useful in foodstuffs, dietary supplements and in pharmaceutical compositions which can then bused to elavate PUFA levels of an animal or plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 TVOTTOMLAGVGITWMVYKVKT--EYKLPCQOSVANLYLAFVIYVTFALLFLOFFVKAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 TLQLAQMVMGVIIGVTVYRIKSSGEY---CQQTWDNLGLCFGVYFTYFLLFANFFYHAYV
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                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                    Length 435;
                                                                                                                                                                                                                                                                                                86; Indels
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                                                                                                                                                                                                                                               36.5%; Score 564; DB 3;
42.0%; Pred. No. 4.4e-53;
iive 45; Mismatches 86,
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Matches 128; Conservative
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Shi Y,

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Nucleic acids encoding 24 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease,
                                                                                                                                                                                                                                                                                                                                                        diabetes mellitus and multiple sclerosis.
                                                                                                                                                                                                                                          Komatsoulis GA, Soppet DR,
                                                                                                                          08-NOV-2000; 2000WO-US030629.
                                                                                                                                                           12-NOV-1999; 99US-0164825P.
                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                         WPI; 2001-374441/39.
                                                              WO200134643-A1
                                Homo sapiens.
 gene therapy.
                                                                                              17-MAY-2001,
                                                                                                                                                                                                                                            Ruben SM,
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                                                                                                                                                                                                                                       New elongase polypeptides which are functional long chain polyunsaturated fatty acid (PUFA) elongase polypeptides are described. The elongase catalyses an elongase reaction to produce PUFA (a 24 carbon fatty acid with at least 4 double bonds) such as di-homo-gamma-linoheic acid (20:3Delta8,11,14), arachidonic acid (20:4Delta5,8.11,14), cocosatentancic acid (20:4Delta5,8.11,14), docosatentancic acid (22:3Delta5,8.11,14), docosatentraenoic acid (22:3Delta7,10,13,16,19), docosatentraenoic acid (22:5Delta7,10,13,16,19), puFA produced is useful in foodstuffs, dietary supplements and in pharmaceutical compositions which can then be used to elavate PUFA levels of an animal or plant
                                                                                                                            Novel isolated polypeptide comprising functional long chain polyunsaturated fatty acid (PUFA) elongase of Caenorhabditis elegans used to produce PUFA for foodstuff, dietary supplement or pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein, proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS, autoimanne disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 SITISVLYFILIKVIQKFWENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 GFYKTLCYSCNPTDVAAFWSFAFALSKIVELGDTWFIILRKRPLIFLHYYHHAAVLIYTV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GFIXSICLAVNPRSPSAFWACMPALSKIABFGDTWFLVLRKRPVIFLHWYHHAVVLILSW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 HSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSWTVTTVQTTQMLAGVGIT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 HAAIBLTAPGRWPIFMAYLVHSIMYTYYAITSIGYRXPKIVSMTVTFLQTLQMLIGVSIS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 G------NLK--ACDXLLLAWNGFLAVFSINGTWRFGIEFYDAVFX 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERFKVWTGNNETIIYSPEYDSTLLIBSCRCTY------QLLILLRQIYYRDIWSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 BLABFWNDLNTPTIYGPNHTDMT---TKYKYSYHFPGZQVADPQYWTILFQKY----WYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 CIVLYLKUNGEM-CQQSYDNLALSFGIYASFLVL-SSFFNNAYLVKKDKK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene 1 encoded secreted protein fragment, SEQ ID NO:163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.4%; Score 547; DB 3; Length 269; 42.4%; Pred. No. 1.7e-51; tive 39; Mismatches 88; Indels 4
                                                                                                                                                                                                             Disclosure; Page 27; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE04173 standard; protein; 270 AA
18-FEB-2000; 2000GB-00003869.
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Les 123; Conservative
                               (UYBR-) UNIV BRISTOL
                                                                                              WPI; 2000-647074/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 269 AA;
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                                                                                                                                                                               composition.
                                                                 Napier JA;
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AMONGHOWANDOMATOR represent CDNAS corresponding to 24 human secreted protein genes, and AAE04100-AAE004170 represent the proteins they encode. AAE041101-AAE04100-AAE004170 represent the protein tragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. The secreted profetines can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, based on the tissues in which they are most highly expressed, and include caveloping products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities. Caveloping products for the diagnosis or treatment of proliferative disorders, diseases of the immune system, AIDS, autoimmune constitute disorders, diseases of the immune system, AIDS, autoimmune disorders, diseases of the immune system, AIDS, autoimmune constitute disorders, schizophrenia, skin disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, skin disorders, endocrine disorders, and infections. The programmy related disorders, and costlers of sorders, and contine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in disonsett of immunosasays e.g., additional mensent sequence represente a human secreted protein fragment referred to present sequence represente a human secreted protein fragment referred to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Disclosure; Page 7; 532pp; English.
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97; Conservative
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Human, receptor and membrane-associated protein; REWAP; atherosclerosis; cardiovascular disorder; hypertension; congestive heart failure; oedema; aneurysm; angina pectoris; ischaemic heart disease; lung disease; nansea; rheumatic heart disease; chronic obstructive pulmonary disease; anaemis; emphysema; bronchitis; gastrointestinal disorder; peptic ulcer; asthma; Crohn's disease; lipid metabolism disorder; Rabry's disease; dementia; pancreatitis; diabetes mellitus; hyperlipidaemia; autoimmune disorder; inflammatory disorder; neurological disorder; Creutzfeldt-Jakob disease; cell proliferative disorder; neurological disorder; disorder; disorder; adisease; protein replacement therapy; adenocarcinoma; Parkinson's disease; multiple sclerosis; Cushing's syndrome; anxiety, schizophrenia, Addison's disease; endocrine disorder; gene therapy; gout; amnesia; cancer; leukaemia; lymphoma; myeloma; sarcoma.
MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYI---IKSSK 283
                    210 MFVGAIVSILTYIWRQDQ--GCHTTMEHLFWSFILYWTYFILFAHFFCQTYIRPKVKAKT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human receptor and membrane-associated proteins and polynucleotides, useful for diagnosing, treating or preventing cardiovascular disorders (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB, Gandhi AR, Burford N;
r J, Yao MG, Lal PG, Tang TY;
Policky JL, Xu Y, Honchell CD;
tran DAM, Gietzen KJ, Hillmann JL;
Tran UK, Richardson TW;
JD, Marcus GA, Zingler KA;
                                                                                                                                                                                                                                                                                                   Human receptors and membrane associated protein REMAP-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 190-191; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L, Nguyen I
3, Ramkumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azimzai Y, Yue H, Ding L, Nguyen Thangavelu K, Elliott VS, Ramkumar Swarnakar A, Warren BA, Walia NK, Au-Young J, Baughn MR, Duggan BM, Raumann BE, Lu Y, Sapperstein SK, Emerling BM, Hafalia AJA, Burrill
                                                                                                                                                                                               ABG92079 standard; protein; 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2001; 2001US-0269580P. 09-APR-2001; 2001US-0282679P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2001; 2001US-0288295P.
14-JAN-2002; 2002US-0348687P.
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                                                                                                                                                                                                                                                                     (first entry)
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E, Gorvard AE;
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                                                                                                          KSQ 270
                                                                        284 KSK 286
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Kable AE,
                                                                                                                                                                                                                                   ABG92079;
                                                                                                                                                                              ABG92079
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The present invention relates to a new receptor and membrane-associated protein (REMAP). The polypeptide, polymucleotide and agonist are useful for treating a condition associated with decreased expression of functional REMAP. The antagonist is useful for treating a disease associated with overexpression of functional REMAP. The anti-REMAP

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contibody is useful for diagnosing a condition or disease associated with the expression of REMAP. These polypeptides, polynucleotides, agonists and antagonists are particularly useful for diagnosing, treating or preventing cardiovascular (e.g. atherosclerosis, hypertension, aneuryems, congestive heart failure, angina pectoris, or ischaemic or rheumatic confessive, lung (e.g. oedema, chronic obstructive pulmonary disease, emphysema or bronchitis) gastrointestinal (e.g. nausea, peptic ulcer or crohn's disease, lipid metabolism (e.g. Rabry's disease, diabetes or crohn's disease, intelmmune/inflammatory (e.g. anaemia, cathma, gout, pancreatitis or Crohn's disease, neurological (e.g. demontia, stroke, Alzheimer's disease, creutzfeldt-Jakob disease, cantingle sclerosis, Parkinson's disease, anxiety, schizophrenia or manssia), metabolic (e.g. Addison's disease), developmental (e.g. cancers including adenocarine or cell proliferative disorders (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, myeloma or cancers including adenocarcinoma, leukaemia, lymphoma, myeloma or cell protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 FOKYWYHSITISVLYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 MFVGAIVSILTYIWRQDQ--GCHTTMEHLFWSFILYMTYFILFAHFFCQTYIRFKVKAKT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis; purp, disorder; cardiovascular disorder; articular cartilage degradation; peripheral vascular disease; atherosclerosis; coronary artery disease; inflammatory disorder; pancreatitis; asthma; gastrointestinal disorder; acne; Sjogren's syndrome; body weight disorder; cerebrovascular disease; acute respiratory distress syndrome; hypercholesterolaemia; alcoholism; postviral fatigue; psychiatric disorder; pre-menetrual syndrome; eczema Alzheimer's syndrome; hypertriglyceridaemia; cystic fibrosis; anorexia; autoimmune disorder; peshchxia; viral disease; anorexia; autoimmune disorder; pascheri, cacharia; viral disease; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 GTVLITGGLKQTVCFINFIDNSTVKFWSWVFLLSKVIBLGDTAFILLKKRPLIFIHWYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTUSAMGYRLPKWVSMTVTTVQTTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    31.8%; Score 492; DB 5; Length 270; 39.9%; Pred. No. 2e-45; ive 53; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dyslipidaemia; atopic disorder; diabetes; ELG6.
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Best Local Similarity 39.99
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 KSK 286
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 270 AA;
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The invention relates to movel elongase polypeptides, genes and their control regions. Sequences of the invention are used in the diagnosis and treatment of polymisaturated fatty acid (PPIPA) disorders such as cardiovascular disorders (e.g. sinusitis, pancreatitis, asthma, osteoarthrisis, rheumatorid arthritis, acne), Sjogren's syndrome, body weight disorders (e.g. obesity, cachexia and anorexia), viral diseases and postviral fatigue, gastrointestinal disorders, eczema, psychiatric disorders, cancer, congenital liver disease, alcoholism, Alzheimer's syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome, syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome, hypercholesterolaemia, hypertriglyceridaemia, dyslipidaemia, peripheral vascular disease, cerebrovascular disease, autoimmume disorders, acute respiratory distress syndrome, atopic disorders, articular cartilage degradation, diabetes and diabetic complication. The present sequence is human elongase (ELG6) protein
                                                                                                                                                                                                      Novel elongase polypeptide, genes and their control regions useful in determining compositions for treating polyunsaturated fatty acid disorder e.g. cardiovascular, inflammation, gastrointestinal disorders and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POKYWYHSITISVLYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 IRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSIMYTYYTTVSAMGYRLPKWVSMTVTTVQTTQ 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTPAILFIQFFVKAYI---IKSSK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYLVYTSFGYKNKVPAGGWFVTMNFGVHAIMYTYYTLKAANVKPPKMLPMLITSLQILQ
                                                                                                   De Antueno RJ, Jenkins DK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 270;
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                                                                                                 Haardt M, De Antuer
ton A, Goldberg YP;
                                                                                                                                                                                                                                                                             Claim 14; Page 160-161; 173pp; English.
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                                                                                                                     Ponton A,
29-NOV-2001; 2001WO-CA001705
                               29-NOV-2000; 2000US-0253728P
                                                                  (XENO-) XENON GENETICS INC
                                                                                                    Knickle LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                 Allen SJ,
                                                                                                                                                    WPI; 2002-547693/58.
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                                                                                                    Winther MD,
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The present invention describes novel human proteins designated NOVX (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrotein xinase elike protein; NOV2a dare keratin 4-like protein; NOV2a is a collagan-like protein; NOV4 is a cystatin B-like protein; NOV9 is a cystatin B-like protein; NOV9 is a matrilin-like protein; NOV9 is a natrilin-like protein; NOV9 is a leukocyte surface antiqen (CD53)-like protein; NOV7 is a natrilin-like protein; NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic, anticipate at tyrosine kinase-like protein. NOVX sequences have cytostatic, anticipate at the protein; and consider a tyrosine kinase-like protein. NOVX sequences have cytostatic, anticipate and immunosuppressive and convergence can be used in therapeutics, particularly for treating, the NOVX sequences can be used in therapeutics, particularly a human. These disorders include cardiomyopathy, atherosclerosis, a disorder related to cell signal processing and metabolic pathway modulation or diabetes. The NOVX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX sequences are also useful for determining the presence of or produced and also associated with altered levels of or nucleic acid, particularly and in the treatment of complastic or neurological disorders, and in the treatment of administration and in the treatment of response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft protein from the present invention. NOV6b is located to chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alsobrook JP, Lepley DM, Burgess CE, Mishra V;
Ji L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA;
Gerlach V, Macdougall J, Stone D, Gunther E, Bllerman K;
cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS; metabolic pathway modulation; neoplastic; neurological disorder; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; crohr's disease; multiple sclerosis; Graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NOVX polypeptides and polynucleotides, useful for treating or preventing a NOVX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
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2000US-0240637P.
2000US-0240648P.
2000US-0240662P.
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2001US-0262455P
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tes 97; Conservative
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N-PSDB; ABNB6919.
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                                                                                             chromosome 10
                                                                                                                                        Homo sapiens.
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Kekuda R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edinger S,
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Matches
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Human, NOVX, cytostatic, antiarteriosclerotic, cardiovascular, lymphoma, antidiabetic, immunosuppressive, neuroprotective, gene therapy, cancer,

Human NOV6b protein sequence SEQ ID NO:20.

(first entry)

29-JUL-2002

52; 227pp; English.

Claim 1; Page

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166
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                                                                                                                                                                                                                                                STVLVYTSFGYKKKVPAGGWFVTWNPGVHAIMYTYYTLKAANVKPPKMLPMLITSLQILQ 209
                                                                                                                                                                                                                                                                                                                        MEAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVTFALLFIQFFVKAYI---IKSSK 283
                                                                                                                                                                                                                                                                                                                                                        FOKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
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, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer; cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS; metabolic pathway modulation; neoplastic; neurological disorder; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; crohn's disease; multiple sclerosis; Graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
                            AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ
                                                                                                        LRSLYAEGFYKTLCY-SCNPTDVAAFWSFARALSKIVELGDTWFIILRKRPLIFLHYYHH
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s RA, Zerhusen BD, S
Stone D, Gunther E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOV6a protein sequence SEQ ID NO:18.
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Li L, Padigaru M, Shimkets
Gerlach V, Macdougall J, S
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16-OCT-2000) 2000US-024664F9.

16-OCT-2000) 2000US-0240648P.

16-OCT-2000) 2000US-0240662P.

16-OCT-2000) 2000US-0240669P.

16-OCT-2000) 2000US-0240703F.

16-OCT-2000) 2000US-0240703F.
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(MILL/) MILLET I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          KSK 286
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Kekuda R, I
Edinger S,
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The present invention describes novel human proteins designated NOVX (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like protein; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like protein; NOV5 is a serotonin receptor-like protein; NOV6 is a matrilin-2-like protein; NOV9 is a matrilin-2-like protein; NOV9 is a matrilin-2-like protein; NOV9 is a land NOV5 sequences have cytostatic, antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and neuroprotective activities, and can be used in gene therapy. The NOVX sequences can be used in therapeutics, particularly for treating, cardiowypathy, atherosclerosis, a discorder related to cell signal cardiomypathy, atherosclerosis, a discorder related to cell signal cardiomypathy, atherosclerosis, a discorder related to cell signal processing and metabolic pathway modulation or diabetes. The NOVX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX pedisposition to a disease associated with altered levels of not propertied or mucleic acid, particularly cancer. The NOVX sequences are especially useful in therapeutic or prophylactic applications for morphasitic or neurological disorders, near in a minimum elementary cancer inmine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 LRSLYAEGFYKTLCY-SCNPTDVAAFWSFAPALSKIVELGDTMFIILRKRPLIFILHYYHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, AIDS, atthma, Crohn's disease, multiple sclerosis or Graft versus host disease. The present sequence represents the human NOV6a protein from the present invention. NOV6a is located to chromosome 10
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Matches 97; Conservative
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WPI; 2002-636596/68.
N-PSDB; ABZ22162, ABZ22164, ABZ22165.
                                                                                                                                                                                                                                                                                                                                               ABB82960 standard; protein; 270 AA.
                                                                                                      Claim 25; Fig 2; 128pp; English.
                            07-FEB-2002; 2002WO-EP001262
                                      08-FEB-2001; 2001US-0267135P
                                                                                                                                                                                                                   97; Conservative
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             KSK 286
                                                                                                                                                                                                                                                                                                                       KSQ 270
                                                (FARB ) BAYER AG.
                                                                                                                                                                                                Sequence 270 AA;
         WO200262974-A2.
Homo sapiens.
                  15-AUG-2002
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                                                          Zhu Z;
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The present sequence represents a human elongase HSELO1-like protein (I).

(I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic, antiparkinsonian, neuroprotective, tranquilliser, antimigraine, and present an elongarkinsonian, neuroprotective, tranquilliser, and can be used in gene therapy. (I) can be used in the treatment of a disease, such as cancral nervous system (CKS) disorder, sathma, metabolic disease or COPD. The human elongase HSELO1-like protein is useful in preventing, treating or ameliorating the diseases cited above, including Parkinson's disease, dementia, multiple solerosis, stroke, HIV, including Parkinson's disease, dementia, multiple solerosis, stroke, HIV, con control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STYLVYTSFGYKNKVPAGGWPVTWRFGVHAIMYTYYTLKAANVKPPKMLFMLITSLQILQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POKYWYHSITISVLYPILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYI---IKSSK 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
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39.9%; Pred. No. 2e-45;
iive 53; Mismatches |
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(first entry)

14-APR-2003

ABB82960;

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The invention relates to identifying a candidate p53 pathway modulating agent that involves assaying a purified LCE (long chain fatty acyl elongase) polypeptide or nucleic acid or its functionally active fragment or derivative, with a test agent. The methods are useful for identifying a candidate p53 pathway modulating agent, modulating a p53 pathway of a candidate p53 pathway modulating agent, modulating a p53 pathway of a candidate branching morphogenesis modulating agent, and modulating branching morphogenesis in amamalian cell. The diseases that can be diagnosed are breast, colon, lung or ovary cancer having greater than 25% expression level. The method is useful for manufacturing a medicament for diagnosing or treating breast, colon, lung or ovary cancer. Sequences ABB82959-966 represent human LCE related polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 POKYWYHSITISVLYFILIKVIQKEMENRKPPTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 GTVLITGGIKQTVCFINFIDNSTVKFWSRVFLLSKVIELGDTAFIILRXRPLIFIHWYFH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFALLFLQFFVKAYI---IKSSK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a candidate p53 pathway modulating agent for diagnosing/treating cancer comprises detecting a test agent-biased activity of an assay system comprising a purified long chain fatty acylelongase (LCE) polypeptide or nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 MFVGAIVSILTYINRQDQ--GCHTTMEHLFWSFILYMTYFILFAHFFCQTYIRPKVXAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 LRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 AAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ
                                                                                                                                                                                                                                                                                                                                                               Funke
                                              LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                               Francis-Lang H,
              Human LCE related protein (sequence ID No. 10)
                                                                                                                                                                                                                                                                                                                                                                 HD, Belvin M,
Koblizek TI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 60-61; 69pp; English.
                                                                                                                                                                                                                                        05-JUN-2001, 2001US-0296076P.
10-OCT-2001, 2001US-0328605P.
15-FEB-2002, 2002US-0357253P.
01-MAR-2002, 2002US-0361196P.
                                                                                                                                                                                                          03-JUN-2002; 2002WO-US017739
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Best Local Similarity 39.99
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Plowman GD,
                                                                                                                                                                                                                                                                                                                                                Friedman L, Pic...
                                                                    cancer; human; enzyme
                                                                                                                                                                                                                                                                                                                                 (EXEL-) EXELIXIS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 270 AA;
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                                                                                                      Homo sapiens.
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210 MFVGAIVSILTYIWRQDQ--GCHTTWEHLFWSFILYMTYFILFAHFFCQTYIRPKVKAKT 267
                                                                                                                                                                                                                                                                                                        Blongase; GLELO; polyunsaturated fatty acid; eicosatetraenoic acid; dihomo-gamma-linolenic acid; transgenic plant; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids encoding elongase enzymes for producing polyunsaturated fatty acids that can be used to form nutritional
                                                                                                                                                                                                                                                                      Putative Drosophila melanogaster homologue of elongase GLBLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thurmond J,
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "unidentified residue"
                                                                                                                                                                                                                                                                                                                                                                                                 Key Location/Qualifiers Misc-difference 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 15, Fig 41, 210pp, English.
                                                                                                                                                                AAY79263 standard; protein; 278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US019715
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                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-237881/20
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                                    KSK 286
                                                                       268 KSQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200012720-A2
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                                                                                                                                                                                                    AAY79263;
                                        284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to identifying a candidate p53 pathway modulating agent that involves assaying a purified LCE (long chain fatty acyl elongase) polypeptide or nucleic acid or its functionally active fragment or derivative, with a test agent. The methods are useful for identifying a candidate p53 pathway modulating agent, modulating a p53 pathway of a cell, or a mammalian cell, diagnosing a disease in a patient, identifying a candidate branching morphogenesis modulating agent, and modulating branching morphogenesis in a mammalian cell. The diseases that can be diagnosed are breast, colon, lung or ovary cancer having greater than 25% expression level. The method is useful for manufacturing a medicament for diagnosing or treating breast, colon, lung or ovary cancer. Sequences ABB82959-966 represent human LCE related polypeptide sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYI---IKSSK 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a candidate p53 pathway modulating agent for diagnosing/treating cancer comprises detecting a test agent-biased activity of an assay system comprising a purified long chain fatty acylelongase (LCB) polypeptide or nucleic acid.
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                                                                                                                                                                                     LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                Human LCE related protein (GenBanK Identifier No. GI#17454617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Francis-Lang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L, Plowman GD, Belvin M, Keyes LN, Koblizek TI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 68-69; 69pp; English.
                                          ABB82966 standard; protein; 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2001; 2001US-0296676P.
10-0CT-2001; 2001US-032860SP.
15-PEB-2002; 2002US-0357253P.
01-MAR-2002; 2002US-0361196P.
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Best Local Similarity
'-Loc 97; Conservat
                                                                                                                                                                                                          cancer; human; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EXEL-) EXELIXIS INC.
                                                                                                             (first
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                                                                                                                                                                                                                                             Homo sapiens.
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                                                                               ABB82966;
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       RESULT 11
                         ABB82966
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Kirchner SJ;

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This sequence is that of a putative Drosophila melanogaster homologue, termed DM1, of Mortierella alpina polyunsaturated fatty acid (PUFA) elongase GIELO (See ANY79243). It is the translation of a DNA fragment identified in a database search using GLELO as query. The 2 sequences show 27.2% identity in a 206 amino acid overlap. The invention provides puby alongase nucleotide sequences and polypeptides that are involved in the elongation of PUFAs, such as gamma-linolenic acid. The invention also provides host cells, transgenic plants and transgenic animals expressing an elongase, and methods for production of PUFAs, such as dihomo-gamma-linolenic acid and eicosatetraenoic acid, for use in nutritional, pharmaceutical, cosmetic and animal feed compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 KPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLCYS--CNPTDVAAFWS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 PRFOLRGPLIIWNTILLAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 MITKYKYSYHFPGEQVADP----QYWILLFQKYWYHSITISVLYFILIKVIQKFMENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elongase; polyunsaturated fatty acid; pufa; transgenic plant; transgenic plant; transgenic non-human animal; plant oil; arachidonic acid; nutritional; pharmaceutical; cosmetic; and fate oil; restenosis; angioplasty; AIDS; acquired immunodeficiency syndrome; multiple sclerosis; cachexia, asthma; fill lammacrory skin disease; osteoporosis; kidney stone; canner; eczema; inflammation; rheumatoid arthritis; psoriasis; platelet aggregation; vasodilation; cholesterol reduction; gastrointestinal bleeding.
   FAFALSKIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                    HSLMYTYYTVSAMGYRLPKWVSWTVTTVQTTQMLAGVGI-TWMVYKVKTBYKLPCQQSVA 253
                                                                                                                                                         Isolated nucleic acid sequences encoding elongase proteins, useful in the production of polyunsaturated fatty acids, e.g. arachidonic acid, which can then be used nutritional compositions and pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated nucleic acid sequences encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leonard AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parker-Barnes JM,
                                                                                                                                                                                                                                               254 NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                      Example 15; Fig 41; 271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU87829 standard; protein; 278 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fruitfly GLELO homologue DM1
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11-JUL-2001; 2001US-00903456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pereira SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-172011/22.
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Thurmond J,
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                                                                                                                                                                                                                                                                                               135 FAFALSKIVELGDTWFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                                                                                                                                                                                    62
useful for inhibiting platelet aggregation, inducing vasodilation, reducing cholesterol, reducing or preventing gastrointestinal bleeding and side effects of non-steroidal anti-inflammatory drugs. The present sequence represents an elongase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                              solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                         123 WLFVLSKLPELGDFIFIVLRKQPLIFLHWYHHITVLIYSWFSYTEYTSSARWFIVMNYCV
                                                                                                                                                                                                                                77 KPFTLKYPLILWNGALAAFSIIATLRPSIDPLRSLYAEGFYKTLCYS--CNPTDVAAFWS
                                                                                                                                                                                                                                                                                                                                                            HSLMYTYYTVSAMGYRLPKWVSMTVTTVQTFQMLAGVGI - TWMVYKVKTEYKLPCQQSVA
                                                                                                                                                                      23 MITKYKYSYHFPGEQVADP----QYWTILFQKYWYHSITISVLYFILIKVIQKFMENR
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                       17;
                                                                                                        Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, SEQ ID NO 7722; 21pp + Sequence Listing; English
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 7722
                                                                                                           DB 5;
                                                                                                        31.4%; Score 485.5; DB 5
37.7%; Pred. No. 1.1e-44;
ive 54; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                      NLYLAFVIYVTFAILPIQPFVKAYIIKSSKKSK 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB60310 standard; protein; 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
                                                                            Seguence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL04413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001,
                                                                                                                                       103;
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ABB60310
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                                                                                                                                                                                                                                                                                                                                                                                                  PAFALSKIVELGDTWFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                                                                                                                                                                                96
                                                                                                                                                                                                                           26
                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL36175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                MITKYKYSYHFPGEQVADP----QYWIILFQKYWYHSITISVLYFILIKVIQKFMENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; very long chain fatty acid biosynthesis enzyme; VLFA; VLCFABE; non-insulin dependent diabetes mellitus; NIDDW; adresnleukodystrophy; ALD; autosomal dominant macular dystrophy; addW; Alzheimer's disease; coronary heart disease; stroke; myocardial infarction; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain fatty
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule comprising a very long chain fatt acid biosynthesis enzyme nucleic acid, useful for treating a disease associated with the biosynthesis enzyme nucleic acid.
                                                                                                                                                                 17;
                                                                                                                                    Length 313;
                                                                                                                                                                   Indels
                                                                                                                                    Query Match 31.4%; Score 484.5; DB 4;
Best Local Similarity 37.7%; Pred. No. 1.6e-44;
Matches 103; Conservative 54; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human VLCFABE MOOSE00004 protein from ctg13284.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NINLSIAMYSSYFVLFARFFYKAYLAPGGHKSR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE37330 standard; protein; 263 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-2002; 2002WO-IB004610.
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                                                                                                         Sequence 313 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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invention relates to very long chain fatty acid (VLPA) biosynthesis

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                              (ALD)
    Sequences
enzymes (VLCFABE) and polynucleotides encoding such proteins. Sequences of the invention are useful for treating VLCFABE diseases such as non-insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD) autosomal dominant macular dystrophy (admb), Adrahimer's disease and coronary heart diseases such as stroke and myocardial infarction. They are also used in gene therapy. The present sequence is human VLCFABE
                                                                                                                                                                                                                                                                                               TMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYTYYTVSAM
                                                                                                                                                                                                                                                                                                                                                                                                               29 YSYHPPGEQVADPQYWTILFQXYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILW
                                                                                                                                                                                                                                                                          89 NGALAAFSIIATLRFSIDPLRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGD
                                                                                                                                                                                                                                                                                                                                                                                                208 GYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVTFAI
                                                                                                                                                                                   Gaps
                                                                                                                                                                                   13;
                                                                                                                                                    Length 263;
                                                                                                                                                                                   Indels
                                                                                                                                                       DB 6;
                                                                                                                                                      31.3%; Score 483.5; DB 6; 37.5%; Pred. No. 1.6e-44; iive 55; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 LFIQFFVKAYI---IKSSKKSKSVKNE 291
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                                                                                                                                                                                     Conservative
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Search completed: June 16, 2004, 15:27:31 Job time : 62 secs

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June 16, 2004, 15:29:04; Search time 48 Seconds (without alignments) 1707.965 Million cell updates/sec
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1545
1 MBLABFWNDLNTFTIYGPNH.....FFVKAYIIKSSKKSKSVKNB 291
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1: /cgm2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgm2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*

2: /cgm2_6/ptodata/2/pubpaa/NEG_NEW_PUB.pep:*

4: /cgm2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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6: /cgm2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

7: /cgm2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

8: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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11: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

13: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

14: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

15: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

16: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

17: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query	Query Match Length DB	D3	ID	Description
1 1				1 1		
-1	1545	700.0	767	4	US-10-369-493-5831	Seguence 5831, Ap
7	492	31.8	270	10	US-09-976-782-18	Sequence 18, Appl
m	492	31.8	270	10	US-09-976-782-20	Sequence 20, Appl
4	492	31.8	270	16	US-10-433-238-9	
'n	485.5	31.4	278	σ	US-09-903-456-58	Sequence 58, Appl
9	485.5	31.4	278	14	US-10-156-911-58	Sequence 58, Appl
7	485.5	31.4	278	14	US-10-408-736-56	
80	479	31.0	271	σ	US-09-903-456-53	•
σ	479	31.0	271	10	US-09-976-782-107	Sequence 107, App
10	479	31.0	271	14	US-10-156-911-53	Sequence 53, Appl
11	479	31.0	271	14	US-10-408-736-50	Sequence 50, Appl
12	479	31.0	272	σv	US-09-903-456-24	Sequence 24, Appl
13	479	31.0	272	14	US-10-156-911-24	Sequence 24, Appl
14	479	31.0	272	14	US-10-408-736-21	Sequence 21, Appl
15	476.5	30.8	261	σ	US-09-903-456-60	~

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61 LYPILIKVIQKEMENRKPFTLKYPLILMNGALAAFSILATLRFSIDPLRSLYAEGFYKTL

8 8 6 8

Sequence 60, Appl Sequence 106, Appl Sequence 110, Appl Sequence 110, Appl Sequence 223, Appl Sequence 233, Appl Sequence 233, Appl Sequence 64, Appl Sequence 64, Appl Sequence 1115, Appl Sequence 1115, Appl Sequence 1114, Appl Sequence 55, Appl Sequence 56, Appl Sequence 62, Appl Sequence 63, Appl Sequence 243,	IN PLANTS FOR PRODUCTION	Length 291; Indels 0; Gaps 0; OYWTILFOXYWYHSITISV 60                         OYWTILFOXYWYHSITISV 60
US-10-156-911-60 US-10-408-736-58 US-09-976-782-106 US-09-976-782-110 US-09-976-782-110 US-09-976-782-110 US-09-976-782-110 US-09-976-782-110 US-09-976-782-109 US-09-976-782-109 US-10-166-911-64 US-10-166-911-64 US-10-976-782-109 US-09-976-782-108 US-09-976-782-108 US-09-976-782-108 US-09-976-782-108 US-09-976-782-108 US-09-976-782-108 US-09-976-782-108 US-09-976-782-108 US-09-973-456-55 US-09-973-456-56 US-09-973-456-62 US-10-156-911-56 US-10-156-911-56 US-10-166-911-56 US-10-166-911-67	ALICHMENTS  US/10369493 575A1 1 C. 1 C. 7 J. 8 SION OF MICROBIAL PROTEINS 18 WITH IMPROVED PROFERTIES 12 B 1-02-28 US 60/360,039 1-21 44	; Score 1545; DB 15; ; Pred. No. 1.7e-152; 0; Mismatches 0; I NHTDWITXXXXYHPPGEQVADPQ
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7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 US-10-369-44 ; Sequence ; Sequence ; GENERAL II ; APPLICAN APPLICA	Query Ma Best Loc Matches Qy Db

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APPLICANT: Winther, Michael D
APPLICANT: Knickle, Leah C
APPLICANT: Haardt, Martin
APPLICANT: Allen, Stephen J
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ORGANISM: Homo sapiens
US-09-976-782-20
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CURRENT PELLORION NUMBER: US/04/04.13
PRIOR APPLICATION NUMBER: 60/240,113
PRIOR APPLICATION NUMBER: 60/240,662
PRIOR APPLICATION NUMBER: 60/240,662
PRIOR APPLICATION NUMBER: 60/240,662
PRIOR PILING DATE: 2000-10-16
PRIOR PILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,703
PRIOR APPLICATION NUMBER: 60/240,703
PRIOR APPLICATION NUMBER: 60/240,669
PRIOR PILING DATE: 2000-10-16
PRIOR PILING DATE: 2000-10-18
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121 CYSCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEH 180
                                            TAAGREYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITMMVYKV 240
                                                                       30 FEEYWATSFPIALIYIVULAAVGONYMKERKGFNLQGPLILWSFCLAIFSILGAVRANGIM 89
                                                                                                                                Length 270;
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ilarity 39.9%; Pred. No. 8.6e-43;
Conservative 53; Mismatches 87;
                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09976782
Publication No. US20030190715A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 97; Conserv
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; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-09-903-456-58
                                                                                 Query Match
Best Local Similarity 37.7%
Matches 103; Conservative
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US-10-156-911-58
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  APPLICANT: Ponton, Andre
APPLICANT: De Antueno, Roberto J
APPLICANT: Jenkin, Solomon O
APPLICANT: Jenkin, Solomon O
APPLICANT: Maka, Solomon O
APPLICANT: Goldberg, Y Paul
TITLE OF INVENTION: Human Elongase Genes, Uses Thereof, and Compounds for
TITLE OF INVENTION: Wodulating Same
FILE REPERENCE: 330339-00064
CURRENT PELLING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: US 60/253,728
PRIOR APPLICATION NUMBER: US 60/253,728
NUMBER: OF SEQ ID NOS: 58
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39.9%; Pred. No. 8.6e-43;
tive 53; Mismatches 87; Indels
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Patent No. US20020138374A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2001-07-11,
PRIOR PLING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ. ID NOS: 116
SOFTWARE FREISE FREICH WINDOR VERSION 4.00
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Best Local Similarity 39.9%
Matches 97; Conservative
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CRGANISM: human
US-10-433-238-9
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LENGTH: 278
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                                                                                                                                      11 VTPNYSYIFDFENDFINGRIRKWMLENWTWVF----YYCGI-----YKLVIFGGQHFMQNR 62
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                                                                                                        23 MITKYKYSYHFPGEQVADP-----QYWIILFQKYWYHSIIISVLYFILIKVIQKFMENR
                                                      Gaps
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  31.4%; Score 485.5; DB 9; Length 278; 37.7%; Pred. No. 4.3e-42; tive 54; Mismatches 99; Indels 17;
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Length 278;
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CTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-156-911-58
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GENERAL INFORMATION:
APPLICANT: Abboct Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Hennoy, Vung-Sheng
APPLICANT: Pereira, Suzette L.
TITIE OF INVENTION: ELCONGASE GENES AND USES THEREOF
FILE REPRENCE: 6407.US.P4
CURRENT APPLICATION NUMBER: US/10/156,911
CURRENT APPLICATION NUMBER: US 09/693,456
PRIOR PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR PILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 NLYLAFVIYVTPAILFIOFFVKAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 NINLSIAMYSSYFVLFARFFYKAYLAPGGHKSR 275
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ORGANISM: Drosophila melanogaster
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US-09-976-782-107
US-09-903-456-53
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                                                      HSIAMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGI-TWMVXKVKTBYKLPCQQSVA 253
                                                                                                                        PRFQLRGPLIIWNTLLAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
                                PAFALSKIVELGDIMFILLRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
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CTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-408-736-56
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                                                                                                                                                                          NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
                                                                                                                                                                                               243 NINLSIAMYSSYPVLFARFFYKAYLAPGGHKSR 275
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APPLICANT: Parker-Barnes, Jennifer M.
APPLICANT: Parker-Barnes, Jennifer M.
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Thurmond, Jennifer M.
TITLE OF INVENTION: ELONGASE GENES AND USES THE
TITLE REFERENCE: 6407.US.Pl
CURRENT APPLICATION NUMBER: US/10/408,736
CURRENT FILING DATE: 2003-04.04
PRIOR APPLICATION NUMBER: US/9/9/379,095A
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 278
                                                                                                                                                                                                                                                                                             Sequence 56, Application US/10408736 Publication No. US20030177508A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local 9
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APPLICANT: Grosse et al APPLICANT: Grosse et al TITLE OP INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-157
CURRENT APPLICATION NUMBER: US/09/976,782
CURRENT PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,13
PRIOR PLING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,703
PRIOR PLING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,703
PRIOR APPLICATION NUMBER: 60/240,703
PRIOR APPLICATION NUMBER: 60/241,190
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41.6%; Pred. No. 2e-41;
ive 47; Mismatches 87; Indels
Sequence 53. Application US/09903456

Sequence 53. Application US/09903456

Patent No. US20201388741

GENERAL INFORMATION:

APPLICANT: Aboott Laboratories

APPLICANT: Huang, Yung-Sheng

CURRENT FILMS DATE: US/09/903, 456

CURRENT APPLICATION NUMBER: US/09/903, 456

CURRENT PILING DATE: 2001-07-11

PRIOR PILING DATE: 1999-09-02

PRIOR APPLICATION NUMBER: US 09/379, 095

PRIOR PILING DATE: 1999-09-02

NUMBER: OF SEQ ID NOS: 116

SEQ ID NO SEQ ID NOS: 116

SEQ ID NO SEC ID NOS: 116

SEQ ID NO SEC ID NOS: 116

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SEQ ID NO SEC ID NOS: 116
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Best Local Similarity 41.6%
Matches 101; Conservative
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CAGANISM: Mus musculus
US-09-903-456-53
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Gaps

167

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49 OKYWYHSITISVLYFILIKVIQKFMENRKPPTLKYPLILMNGALAAFSIIATLRFSIDPL 108
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                                                                                           32 BEYMVSSFLIVVVYILLIVVGQTYMRTRKSFSLQRPLILMSFFLAIFSILGTLRMWKFMA
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31.0%; Score 479; DB 14; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels
; Pred. No. 2e-41;
47; Mismatches 87; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50, Application US/10408736
Publication No. US20030177508A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
Best Local Similarity 41.6%;
Matches 101; Conservative 4
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; ORGANISM: Mus muculus
US-10-408-736-50
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APPLICANT: Mukerji, Pradip
APPLICANT: Mukerji, Pradip
APPLICANT: Heang, Yung-Sheng
APPLICANT: However
FILE REFERENCE: 6407.US.P4
CURRENT APPLICANTON NUMBER: US/10/156,911
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/903,456
PRIOR APPLICATION NUMBER: US 09/903,456
PRIOR APPLICATION NUMBER: US 09/19,095
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FSELSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.0%; Score 479;
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,637
PRIOR PILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,669
PRIOR APPLICATION NUMBER: 60/262,455
PRIOR APPLICATION NUMBER: 60/262,455
PRIOR APPLICATION NUMBER: 60/240,648
PRIOR FILING DATE: 2001-01-18
PRIOR PELING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 127
SEQ ID NO 107
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 53, Application US/10156911 Publication No. US20030163845A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eur
                                                                                                                                                                                                                                                                                                                                                                                 31.0%;
41.6%;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 41.6%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-782-107
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108

Gaps

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16

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TYPE: PRT
ORGANISM: Mus musculus
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NAME/KEY: VARIANT
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31.0%; Score 479; DB 9; Length 272;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels
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                                                                                                                                                                                 APPLICANT: Mukerii, Fradip
APPLICANT: Honard, Amanda Run-Yeong
APPLICANT: Heonard, Amanda Run-Yeong
APPLICANT: Heonard, Amanda Run-Yeong
APPLICANT: Hereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USBS THEREOF
FILE REPERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR PILING DATE: 1939-08-03
PRIOR PILING DATE: 1939-08-03
PRIOR FILING DATE: 1938-09-02
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 24
TENUM DATE: 1000: 116
SEQ ID NO 24
TENUM DATE: 1000: 116
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Subjection No. US20030163845A1
GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
APPLICANT: Leonard, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Freibre 6407.US.P4
                                                                                                       Sequence 24, Application US/09903456
Patent No. US20020138974A1
GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
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ORGANISM: Mus musculus
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268 SKS 270
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CURRENT PRILATION NAMES: US 09/001,456

PRIOR FILTNO DATE: 2002-10-011

PRIOR PRILATION DATE: 300-10-07.1

PRIOR PRILATION NAMES: US 09/145,628

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PREPICANT: PRINATION NAMES: US 09/145,628

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PREPICANT: PRILATION NAMES: US 09/145,628

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Search completed: June 16, 2004, 15:34:59
Job time : 49 secs
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                                                                                                                                                                                                             49 OKYWYHSITISVLYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL 108
                                                                                                                                                                                                                                                                                                      109 RSLYAEGFYKTLCYSCNPTD-VAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHHA 167
                                                                                                                                                                                                                                                                                                                                     92 TWAFTVGLKQTVCFAIYTDDAVVRFWSFLESKVVBLGDTAFILLRKRPLIFVHWYHHS 151
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                                                                                                                                                                                                                                       32 EEYWVSSFLIVVVYYLLLIVVGGTYMRTRKSPSLQRPLILMSFPLAIFSILGTLRWKFMA 91
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Best Local Similarity 40.2%; Pred. No. 3.4e-41;
Matches 99; Conservative 49; Mismatches 87; Indels 11; Gaps
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31.0%; Score 479; DB 14; Length 272;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indele
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LOCATION: (218)...(218)
CTHER INFORMATION: Xaa = Unknown or Other at position 218
US-09-903-456-60
                      LOCATION: (272)...(272); OTHER INFORMATION: Xaa = Unknown or Other at position 272 US-10-408-736-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Heonard, Amanda Eun-Yeong
APPLICANT: Heonard, Amanda Eun-Yeong
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELDONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/13/9,095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-02
NUMBER OF SOF ID NOS: 116
SOFTWARE: FestSEQ for Windows Version 4.0
SEQ ID NO 60
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. Sequence 60, Application US/09903456
. Patent No. US20020138874A1
. GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
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SKS 270
NAME/KEY: VARIANT
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73 APELIHVLRHYGLPHSVCVPSYIEQDRVCGFWTWLFVLSKLPELGDTIPIVLRKQPLIFL 132
                                               VQTTQMLAGVGI-TWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFALLFIQFFVKAYIIK 280
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C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex C,Accession: T34200
R,Du, Z.; Gattung, S.
Submitted to the EMBL Data Library, November 1995
A,Description: The sequence of C. elegans cosmid D2024.
A,Reference number: Z21488
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1 MELAEFWNDLNTFTIYGPNH......FFVKAYIIKSSKKSKKVKB 291
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length
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3: pir3:*
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	Similarity 100 11; Conservative	MELAEFWND	LYFILIKVI           LYFILIKVI				
	Query Match Best Local S: Matches 291	स स	E 9	121	181	241	RESULT 2 T34200

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A; Map position: 4
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Best Local S:
Matches 83
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C,Species: T20786
R,Matthews, L.
Submitted to the EMB1 Data Library, October 1996
A,Reference number: Z19324
A,Reference number: Z19324
A,Reference preliminary; translated from GB/EMBL/DDBJ
A,Residues: Dealminary; translated from GB/EMBL/DDBJ
A,Residues: 1-274 «MIL»
A,Residues: L-274 «MIL»
A,Residues: L-274 «MIL»
A,Residues: L-274 «MIL»
A,Residues: Coencies: EMB1:Z81058; PIDN:CAB02921.1; GSPDB:GN00022; CESP:F11E6.5
A,Reperimental source: Glone F11E6
C,Genetics:
A,Genetics:
A,Map position: 4
A,Introns: 38/3; 99/1; 183/2; 235/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 GFYKTLCYSCN-PIDVA-AFWSPAFALSKIVBLGDTMFIILRKRPLIFLHYYHHAAVLIY 172
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                                                                                                                                               Length 435;
A,Accession: T34200
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rosidues: 1-435 - GDUZ>
A,Cross-references: EMBL:U41011; PIDN:AAA82288.1; CESP:D2024.3
A,Cross-references: EMBL:3,306/1; 398/3
                                                                                                                                                                                                                  22 DWTTKY---KYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Score 398, DB 2; Length 27;
, Pred. No. 1.2e-27;
48; Mismatches 99; Indels
                                                                                                                                                                                 86; Indels
                                                                                                                                              36.5%; Score 564; DB 2;
42.0%; Pred. No. 4.9e-42;
tive 45; Mismatches 86;
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ilarity 37.1%;
Conservative 4
                                                                                                                                                                   Best Local Similarity 42.0%
Matches 128; Conservative
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Best Local Similarity
Matches 89; Conserva
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                                                                                                                                                     Query Match
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procein F41H10.8 [imported] - Caenorhabditis elegans

() Species: Caenorhabditis elegans

() Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

() Accession: H88690

R; Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biols

A; Reference number: A; A; 800; MUID: 999, 69613; PMID: 985, 91919; PMID: 985, 9195

A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; at A; Molecule type: DNA

A; Residue: 1-274 < STO>

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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 TGPLALMWAGLAIFSTLGSLATTFGLLHEFFSRGFFESYIHIGDFYNGLSGMFTWLFVLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 KIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 YYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVAN----LY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 KYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLCYSCN-PTDVAAFWSFAFALS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291
                                                  216 IPGHLVPIKSADSVPGCAVŠMAVLSIGGLMYISYLFLFAKFFXKAYIQKKS-PTKTSKQB 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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233 ITWMVYKVKTBYKLP-CQQSVANLYLAFVIYVTPAILFIQFFVKAYIIKSSKKSKKVKNE
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A,Map position: 4
A,Introns: 110/1; 238/3
A,Introns: Jaccharomyces probable membrane protein YCR034w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 24.2%; Score 374; DB 2; Length 27 Local Similarity 30.4%; Pred. No. 1.6e-25; nes 83; Conservative 59; Mismatches 111; Indels
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Caenorhabditis elegans

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                                                                                                                                                .08 LRSLYASGFYKTLCYSCNPT-DVAAFWSFAFALSKIVELGDTWFIILRKRPLIFLHYYHH 166
                                                                                                                                                                      167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226
                                                                                                                                                                                                                                                             160 ILFWIYAWYSHPLTPGFNRYGIYLNFVVHAFMYSYYFLRSMKIRVPGPIAQAITSLQIVQ 219
                                                                                                                                                                                                                                                                                                   227 MLAGVGITWWVYKVKTBYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSK-KS 285
                                                                                                                                                                                                                                                                                                                      220 FISCAVLAHLGYLMHFTUNNCDFEPSVFKLAVFMDTTYLALFVNFFLQSYVLRGGKDKY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA92960.1; GSPDB:GN00022; CESP:F56H11.3
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                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein P56H11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27791
R;Wilkinson, J.
submitted to the EMBi Data Library, January 1996
A;Reference number: Z19616
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                                                                                                            PADHEDVIIQASILYKVVVPGTKWFWRNRQPFQLTIPLNIWNFILAAFSIAGAVKWIPEF
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 Length 288;
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Query Match 23.3%; Score 360; DB 2; Length 28
Best Local Similarity 31.3%; Pred. No. 2.9e-24;
Matches 76; Conservative 58; Mismatches 107; Indels
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Nalecule type: DNA
A.Nasidues: 1-281 <WIL>
A.Cross references: EMBL:268749; PIDN:CAA92960.1; GSPD
A.Experimental source: clone F56H11
C.Genetics:
A.Gene: CESP:F56H11.3
A.Map position: 4
A:Introns: 71/3; 132/1; 178/2; 215/2; 266/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.3%; Score 329; DB 2; Best Local Similarity 31.7%; Pred. No. 1.5e-21; Matches 77; Conservative 49; Mismatches 93;
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E88650
protein F41H10.7 [imported] - Caenorhabditis elegans
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Cyperters Carolinal Haston Craylsion 10-May-2001 #text_change 10-May-2001
Cyperters 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
CyAccession: E88690
CyAccession: E88690
Ayritle: Genome sequence of the nemacode C. elegans: a platform for investigating biolo Ayritle: Genome sequence of the nemacode C. elegans: a platform for investigating biolo Ayritle: Genome sequence of the nemacode C. elegans/ and www_sanger.ac.uk/Projects/C_el Ayrocession: E88690
Ayrocession: E88690
Ayrocession: E88690
Ayresidus: preliminary
Ayrocession: E88690
Ayresidus: preliminary
Ayrocession: CyGenetics: GB:chr_IV; PIDN:AAB03174.1; PID:gl397335; GSPDB:GN00022; CESP:F41H1
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A;Experimental source: strain 972h-; cosmid c806
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C;Accession: T37734; T39101
B;Wedier, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
B;Wedier, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
A;Reference number: 221742
A;Reference number: 221742
A;Accession: T37734
A;Accession: T37734
A;Accession: T37734
A;Residues: 1-328 <WED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 AGV-GITWMYYKVKTEYKLPCQQSVANLYLAFVIYYTFAILFIQFFVKAYIIKSSKKSKS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 VAIFAQVHVSYKHYVEGVEGLAYSFRGTAIGFFMLTTYFYLMIQFYKEHYLKNGGKKYNL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITISVLYFILIKVIQKFWENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRS-LYA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 SAKLAVGYIATIFGLKYYMKDRKAFDLSTPLNIWNGILSTFSLLGFL-FFFPTLLSVIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 YTV---HSGAEHTAAGREYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTÇML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A,Introns: 5/2, 125/3
C,Superfamily: Saccharomyces probable membrane protein YCR034w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 327.5; DB 2; Length 32.8%; Pred. No. 2.1e-21; ive 44; Mismatches 109; Indels
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A;Molecule type: DNA
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Hes 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 AKDQ 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Gene: F41H10.7
A, Map position: 4
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Best Local S:
Matches 80,
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GSPDB:GN00066; SPDB:SPAC1B2.03c

    fission yeast (Schizosaccharomyces pombe)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
T50139
T50139
GNS1/SUR4 family protein [imported] - fission yeast (Schizosaccharomyces pom
C;Species: Schizosaccharomyces pombe
C;Species: 09-Jun-2000 Headuence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: T50139
C;Accession: T50139
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: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 VELGDIMFIILRKRPLIFLHYYHH--AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 YKYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFME--NRKPFTLKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 FEYFSGYPAEQFEFIHNKTPLAN--GYHAVSIIIVYYIIIPGGQAILRALNASPLKFKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 LILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLC--YSCNPTDVAAFWSFAPALSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 YYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTEY------KLPCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 345;
                                                                                             A Map position: 12R
C; Superfamily: Saccharomyces probable membrane protein YCR034w
C; Superfamily: Saccharomyces probable membrane protein
C; Keywords: transmembrane protein
F; 69-89; Domain: transmembrane #status predicted <TM2>
F; 110-129; Domain: transmembrane #status predicted <TM3>
F; 209-229; Domain: transmembrane #status predicted <TM3>
F; 243-263; Domain: transmembrane #status predicted <TM4>
F; 283-304; Domain: transmembrane #status predicted <TM5>
F; 283-304; Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.0%; Score 262; DB 2; Length 34: 28.9%; Pred. No. 1.5e-15; ive 53; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 GTQAAAAYGYLILTSYLLLFISFYIQSY----KKGGKKTVKKE 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 QSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKK--SKSVKNE 291
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     A;Gene: SGD:SUR4; SRB1; APA1
A;Cross-references: SGD:S0004364; MIPS:YLR372w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.2<sup>3</sup>
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 28.9
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Best Local S:
Matches 82,
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Ribu, 26

Ribuscription: The sequence of S. cerevisiae cosmid 8039.

A; Reference number: $51377

A; Accession: $51377

A; Rolecule type: DNA

A; Rolecule type: DNA

A; Ribitle: Transcriptional control of yeast plasma membrane H(+)-ATPase by glucose. Clonin A; Richard type: DNA

A; Reference number: $69, 18076-18082, 1995

A; Richard type: DNA

A; Reference number: $69207, 'R', 209-329, 'PY', 332-345 cGAR>
A; Residues: 1-34, 'D', 36-207, 'R', 209-329, 'PY', 332-345 cGAR>
A; Residues: Biophys. Acta 1263, 261-265, 1995

B; Revardel, E.; Bonneau, M.; Durrens, P.; Aigle, M.

B; Revardel, E.; Bonneau, M.; Durrens, P.; Aigle, M.

B; Revardel, E.; Bonneau, M.; Durrens, P.; Aigle, M.

A; Reference number: $59600; MUID:96004900; PMID:7548216

A; Reterence number: $59600

A; Returns: nucleic acid sequence not shown

A; Residues: 1-345 cREW>

B; Residues: 1-345 cREW>

A; Residues: 1-345 cREW>

A; Residues: 1-345 cREW>

B; Residues: 1-345 c
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A;Reference number: 848517
A;Accession: $48517
A;Accession: $48238
A;Dupuy, P.H.; Bonin, O.; Kaghad, M.; Caput, D.; Fe submitted to the EMBL Data Library, October 1994
A;Description: $48238
A;Accession: $48238
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUR4 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L8039.2; protein YLR372w; regulatory protein APA1; SRE1 prote
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
C;Accession: S48517; S48238; S51390; A54902; S53600; S43122; S49468
R;Revardel, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPSICNEKAWTQPLVFLYYCAYISKFLELTDTPFLVLRKKPLQFLHCYHHGATAVLVYTQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 TISVLYFILLIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGF 116
                                                                                                                                                                                                                                                                                                                                                                                                                   117 YKTLCYSCNPTDVAAFWSPAFALSKIVELGDTMPIILRKRPLIFILHYYHH--AAVLIYTV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSGAEHTAAGREYILMNYFAHSLMYTYYTVSAMGYRLP--KWVSMTVTTVQTTQMLAGVG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 IVG--RTSISWLIIEINLLVHVTMYYYYYLVAKGIRVPWKKM----VTRPQIVQFFADLG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITWMVYKVKTEYKLP-----CQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKK 284
                                                                                                                                                                                                                                                                                                                     66
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                         23;
                Length 328;
     th 18.2%; Score 281.5; DB 2; Length Similarity 31.0%; Pred. No. 2.7e-17; 76; Conservative 36; Mismatches 110; Indels
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R;Du, Z.
Query Match
Best Local Similarity
Matches 76; Conserv
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167

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A,Accession: S12016
A,Molecule type: DNA
A,Residues: 1-347 <THI.>
A,Residues: 1-347 <THI.>
A,Cross-references: BMBL:X56909, NID:g4489; PIDN:CAA40226.1; PID:g4490
B,Wicksteed, B.L.; Roberts, A.B.; Sagliocco, P.A.; Brown, A.J.P.
Yeast 7, 761-772, 1991
A;Title: The complete sequence of a 7.5 kb region of chromosome III from Saccharomyces A,Reference number: S40917; MUID:92133166; PMID:1776366
R;Thierry, A.; Fairhead, C.; Dujon, B.
Yeast 6, 521-554, 1990
A;Title: The complete sequence of the 8.2 kb segment left of MAT on chromosome III
A;Reference number: S12916; MUID:91181345; PMID:1964349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 YYVIIFGGRFILSKSKPFKLNGLFQLHNLVLTSLSLTLLLLMVEQLVPIIVQHGLYFAIC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 YSCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH -- AAVLIYTVHSGAE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 HTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVG-ITWMVY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C)Accession: T46257

R)Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000

A;Reference number: 223031

A;Reference number: 223031

A;Reference number: 223031

A;Reference number: 246257

A;Retwies preliminary

A;Residues: 1-158 <AAA>

A;Coss_references: EMBL:AL137506

A;Experimental source: adult amygdala; clone DKFZp7610031

C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 KVKTEYKLP-----CQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSVK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:S78624; NID:9244237; PIDN:AAB21260.1; PID:9244240 R;Dujon, B.; Pairhead, C.; Thierry, A. submitted to the Protein Sequence Database, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A,Molecule type: DNA
A,Residues: 1-347 <DUJ>
A,Cross-references: EMBL:X59720; NID:g1907116; PID:g1907176; MIPS:YCR034w
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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C,Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 3R
C,Superfamily: Saccharomyces probable membrane protein YCR034w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKeywords: transmembrane protein
F)67-84/Domain: transmembrane #status predicted <TM1>
F)10-129/Domain: transmembrane #status predicted <TM2>
F)153-169/Domain: transmembrane #status predicted <TM3>
F)198-214/Domain: transmembrane #status predicted <TM3>
F)236-254/Domain: transmembrane #status predicted <TM4>
F)275-299/Domain: transmembrane #status predicted <TM5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: SGD:S0000630; MIPS:YCR034w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S19446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
A, Residues: 1-347 <WIC>
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane protein YCR034w homolog YUL196c - yeast (Saccharomyces cerevisiae)

Whiternate names: protein J0343; protein YUL196c
C;Species: 3accharomyces cerevisiae
C;Species: 3accharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision
C;Accession: S46638; S5698
R;Purnelle, B.; Coster, F.; Goffeau, A.
R;Purnelle, B.; Coster, F.; Goffeau, A.
A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifie as gene ACO1 and two homologues to chromosome III genes.
A;Reference number: S46621; MUID:95274326; PMID:7754713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
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                                      QTTQMLAGVGITWMVYKVKTEYK----LP----CQQSVANLYLAFVIYVTFAILFIQFFV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LYPILIKVIQKPMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 CNVESWIQPMETLYYLNY---WTKFVEFADTVLMYLKRRKLTFLHTYHGAIALLCYNQL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 AEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ-MLAGVGITWM 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 VYK--VKTEYKCPCQQ-----SVANLYLAFVIYVTFAILFIQFFVKAYIIKS-SKKSK 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Robeidues: 1-310 <PUR>
A;Robeidues: 1-310 <PUR>
A;Cross-references: EMPL:X77688; NID:g1183992; PIDN:CAA54764.1; PID:g547599
R;Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCR521
C;Species: Saccharomyces cerevisiae
C;Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 21-Jul-2000
C;Accession: S12916; 640919; S19446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-310 <PUW>
A;Cross-references: EMBL:Z49471; NID:g1008410; PID:g1008411; MIPS:XJL196c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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C,Superfamily: Saccharomyces probable membrane protein YCR034w
C,Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SGD:ELO1
A;Cross-references: SGD:S0003732; MIPS:YJL196c
                                                                                                                                                                                                                         275 KAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                                                284 NTYÍKRGAKKNÝ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S56977
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Best Local Simi
Matches 66;
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H. A; Atuthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Fraser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: D96693
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-14635 <STO>
A;Cross-references: GB:AE005173; NID:g9755445; PIDN:AAF98206.1; GSPDB:GN00141
C;Genetics:
A;Genetics:
A;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Map position: 1
C,Superfamily: unassigned ATP-binding cassette proteins; ATP-binding
            408, 816-820, 2000
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C;Genetics:
A;Gene: CESP:Y47D3A.14
A;Introns: 17/2; 51/3; 102/3; 169/3; 246/1; 287/2; 319/3; 371/3; 395/2; 440/3; 450/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                        141 KIVELGDTMFIILRKR--PLIFLHYYHHAAVLIYTVHSGAEHTAA--GRFYILMNYFAHS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 VMYSYYGLSALGPAYQXYLWWKKYLTSEQLVQFVIVALHISQPFFMEDCKYQPPVFACII 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMYTYYTVSAMG--YRLPKWVSMTVTTVQTTQ-MLAGVGITWMVYKVKTBYKLPCQQSVA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALAAPSIIATLRFSIDPLRSLYAEGFYKTLCYSCNPTDVAAFWSFAPALSKIVELGDTM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILLRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFNFRPSHISDRSY---LKEWYYYNCVFQLGLGILMI------PRILTSSLSGWH 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL----PKWVSMTVTTVQTTQMLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis
Cispec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                  14:
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                                                                                                                                                                                         Length 158;
A;Note: DKFZp7610031.1
C;Superfamily: Saccharomyces probable membrane protein YCR034w
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSVKN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSY-SFM----FLLLFLHFWYRAY-TXGQRLPKTVRN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
T31527
hypothetical protein Y47D3A.14 - Caenorhabditis elegans
                                                                                                                                                                            , DB 2;
1.1e-09;
                                                                                                                                                                            12.4%; Score 191; DB
llarity 31.8%; Pred. No. 1.1e
Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| :|: |:|: |:| |: |: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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nes 50; Conserv
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1184 IMTVVIGVLFGLIFWOIGTKTENEODLNNFFGAMYAAVLFLGALNA----ATVOPALAIE 1239
                                                                                                                                                                                                                                                                                                                                                                                                                 1132 ELIKOLST---PPPGSKÖVYFKTKYAQSFSTQTKACFWKQYWS----YWRHPQYNAIRF 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1294 LWFYYYMLTSFIYFTLYGMIMALTPNYQIAGICMSFFLSLWNLFSGFLIPRPQIPIWWR 1353
                                                                                                                                                                                                                                                55 --SITISVLYFILLIKVIQKFMENRKP----FTLKYPLILWNGALAAFSIIATURFSIDPL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 IFLHYYHHAAVLIYTVHS-----GAEHTAAG----RFYILMNYFAHSLM-----Y 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 TYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYK------LPCQQ 250
                                                                                                                                                                                                                                                                                                                                                                          RSLY----AEGFYKTLCYSCNPTDVAAFWS-----FAFALSKIVBLGDTMFIILRKRPL
                                                                                                                         5 SEWNDINTETIYGPNHTDMTTKYKYSYHFPGEQVAD--PQYWTILFQKYMYH-----
                                                                 Gaps
                                                              87;
                                                              Indels
7.6%; Score 117.5; DB 2;
21.8%; Pred. No. 0.037;
trive 55; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 SVANLYLAFVIYVTFAILFIQFFVKAYIIK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: June 16, 2004, 15:29:33
Query Match
Best Local Similarity 21.8<sup>†</sup>
Matches 72, Conservative
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cassette homology

Q8i251 plasmodium Q7zxj4 xenopus lae

5 <u>2.</u>

r<sup>i</sup>A

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Osizvi plasmodium
Oguris schizosacch
Ogblro leishmania
Ozrus brachydanio
Qaschyd dictyosteli
Ogms02 drosophila
Oguple drosophila
Oguple drosophila
Oyuc3 brachydanio
                                                                                                                                                                                                                     Q8jzv3 mus musculu
Q8jzv3 mus musculu
Q8avg1 xenopus lae
Q7svn0 brachydanio
Q9vh56 drosophila
Q8byy8 mus musculu
Q9j5f5 fowlpox vir
Q9dzy9 mus musculu
Q8dzy9 mus musculu
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Ogbhqg leishmania
Ogbhqg leishmania
Ogvczo drosophila
Ogwczo homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.7%; Score 659.5; DB 5; Length 286; Best Local Similarity 45.1%; Pred. No. 2.4e-50; Matches 130; Conservative 51; Mismatches 88; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Socience 282:2012-2018(1998).

EMBL; A112294; CAB61069-11; -.
WormPep; Y33F4B.2; CE22388.

GO; GO:0016021; C:integral to membrane; IRA.

InterPro: IPRO02076; GNSI_SUR4.

PROSITE; PS01188; ELO; 1.

PROSITE; PS01188; ELO; 1.

SEQUENCE 286 AA; 33402 MW; DF9DB8D3B2F1C479 CRC64;
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es 88; Indels
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Last sequence update)
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                                 Q812V3
Q9UR34
Q9BLR0
Q7ZTU5
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Q9J5F5
Q9J5F5
Q9BX38
Q9BX38
Q9BLQ9
Q9WE5
Q9WCZ0
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Q9WCZ0
Q9WTY7
                                                                                                                                                                                 07 ZUC3
09 VN 29
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08AVG1
07SY74
07ZVN0
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Q8MS02
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Q9VHX7
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MEDLINE=99069613; PubMed=9851916;
 01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-0TW-2003 (TrEMBLrel. 24,
Y53F4B.2 protein.
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Q802x6 brachydanio
Q92016 rattus norv
Q8ce45 mus musculu
Q9h5j4 homo sapien
Q8ncd1 homo sapien
Q9xvq9 caenorhabdi
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Q9vv87 drosophila
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1 MELAEFWNDLNTFTIYGPNH......PFVKAYIIKSSKKSKSVKNE 291
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Q861t1
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9Z0L5
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Q8CZ16
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Q9H5J4
Q8NCD1
Q8NCD1
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Q8NCD1
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RA MEDULINE-ZOUS GOOG, EACHER S. E., FIGLE R. B., By Addms M.D., Cellniker S. E., FIGLE R. B., Hoskins R.A., Galle R.F.,
SA Amanatides P.G., Scherer S. E., Li P.W., Hoskins R.A., Galle R.F.,
SULCON G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L. X.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L. X.,
String G.G., Worthan J.R., Panell M.D., Zhang Q., Chen L. X.,
R. Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
R.A. Abril J.F., Agbayani A., An H.J., Andrews-Pfaunkoch C., Baldwin D.,
R.A. Ballew R.M., Basu A., Baxendale J., Baytaktargolu L., Beasley B.M.,
R.A. Besson K.Y., Bence P.V., Barman B.P., Bhandari D., Bolshakov S.,
R.A. Borkova D., Botchan M.R., Buuck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botchan M.R., Buuck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botchan M.R., Buuck J., Brokstein P., Brottier P.,
R.A. Challos S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R.A. Durbin K.J., Evarpelista C.C., Retraz C., Ferriera S., Fleischmann W.,
R.A. Barkov B., Bornellian A.E., Garelli J. H., Gu Z., Chan P., Harris M.,
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Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Jalali M., Kalush P., Wurphy B., Murphy L., Murry D.M., Nelson D.L.,
Rockin D.R., Moleon Y.A., Nixon Y., Murry D.M., Nelson D.L.,
Rasko P., Lei Y., Levitesy A.A., Li J., Li Z., Liang Y., Lin X.,
Mulliams S.M., Noy M., Murphy B., Murphy L., Murry D.M., Nelson M.,
R.A. Balazzolo M., Pittenan G.S., Pan S., Pollard J., Puri V., Shen H.,
R. Balazzolo M., Pittenan G.S., Pan S., Pollard J., Puri V., Shen H.,
R. Balazzolo M., Pittenan G.S., Pan S., Pollard J., Puri V., Shen H.,
R. Balazzolo M., Pittenan G.S., Pan S., Pollard J., Puri V., Shen H.,
R. Balazzolo M., Pitten
                                                                                                                 117 YKTLCYSCNPTDVAAFWSFARALSKIVELGDTMFILLRKRPLIFLHYYHHAAVLIYTVHS 176
                  TISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGF 116
                                             177 GAEHTAAGRFYILANYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWM 236
                                                                                                                                                                                                                                               Oyvory; QGNBS;

O1-MAY-2000 (TrEMBLrel 13, Created)

O1-MAY-2000 (TrEMBLrel 13, Created)

O1-OCT-2002 (TrEMBLrel 25, Last sequence update)

O1-OCT-2003 (TrEMBLrel 25, Last annotation update)

CG3971 protein (Putative multipass transmembrane)

Protein Noa) (LD10431p).

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

BLOSPOTA: Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=20196006; PubMed=10731132;
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A Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Byans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An Genter A., Champe M., Devenport L.B., Dietz S.M.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
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A Gonzalez M., Houck J., Hoskins R.A., Hoskins D., Howland T.U.,
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A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A Pocleb J., Paragas V., Park S., Patel S., Pricifer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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CSTRAINBERKALS.

CA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Champe M., Chavez C., Dorset V., Farfan D., Frise E., George R.,

Champe M., Chavez C., Dorset V., Farfan D., Frise E., George R.,

Champe M., Chavez C., Dorset V., Parkan D., Kungail C.J.,

Conzalez M., Chavis S.E., Rubin G.M., Celniker S.,

Numco J., Pacleb J., Paragas V., Park S.,

Numco J., Pacleb J., Paragas V., Park S.,

La Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; ARE05256; AAF49430.2; -..

EMBL; ARE05256; AAF49430.2; -..

EMBL; ARE05256; AAF49430.2; -..

EMBL; ARE05256; AAF49430.2; -..

EMBL; ARE05266; CANGORDED.

PlyBase; FBgn0036650; Baldspot.

CO: GO:0016411; Poxidoredutase activity; IRA.

CO: GO:0016418; P:electron transport; IEA.

EMPL: ARE05806; Rieske_dom.
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Jung A.G., Schaefer M.A.;
Jung A.G., Schaefer M.A.;
"The non gene encodes a member of a widely distributed family of integral membrane proteins in Drosophila.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 AA; 36829 MW; B741960F28D2A3AD CRC64;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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86 ILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLC-YSCNPTDVAAFWSFAFALSKIVE 144
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                                                                                                                                                                                                                                                                                                                                                                      184 RAAGPRUSRKFAMFITLSQITQMLMGCVINYLVFNWMQHDNDQCYSHFQNIFWSSLMYLS 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 SAMGYREDEKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVT 264
                                                                                                                                                                                                                                      LGDTMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRPYILMNYFAHSLMYTYYTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 NHTDM----TTKYKYSYHPPGBQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NWTDPQLPLTEYBPERHF-DERLAIE--W---MQDNWKKSFLFGAVYVVLVFGGQHFMKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 RKPFTLKYPLILMNGALAAFSILATLRFSIDPLRSLYAEGFYKTLC---YSCNPTDVAAF
                                                                                                                                               26 KYKYSYHPPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q802X6 PRELIMINARY; PRT; 268 AA.
Q802X6;
Q802X6;
Q802X6;
Q802X6;
Q1-UUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-UUN-2003 (TrEMBLrel. 25, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to fatty acid elongase 2.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygali; Neoprerygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TaxID=7955;
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                                                                                   267;
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                                                                                 DB 11; Length
                                                                               ; Score 447.5; DB 11; Length
; Pred. No. 1.2e-31;
50; Mismatches 109; Indels
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                                               4026C9CB33FDDD23 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 YLVLFCHFFFEAYIGKVKKATKA 266
InterPro; IPR002076; GNS1_SUR4
                                              31610 MW;
                                                                               29.0%;
                                                                                                                 97; Conservative
              Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
SEQUENCE 267 AA; 31610
                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                               FAFALSKIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                                                                                                                                                                                                                                                                 HSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGI-TWMVYKVKTBYKLPCQQSVA 253
                                                                                                            8 VIPNYSYIFDPENDFIHQRIRKWMLENWTWVF---YYCGI----YMLVIFGGGHFMQNR 59
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                                                                               23 MITKYKYSYHFPGEQVADP-----QYWTILFQKYWYHSITISVLYFILIKVIQKFMENR
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acyl elongase (Long-chain fatty-acyl elongase) (Myelination associated SUR4-like protein).
ELOVIG OR FAD OR LCE OR MASR.
Mus misculus (Mouse).
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Matsuzaka T., Shimano H.;
"murine complete cds for new fatty acyl elongase similar to cig30
(U97107).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=21576178; PubMed=11567032; Marrington J.A., Horton J.D., Moon Y.A., Shah N.A., Mohapatra S., Warrington J.A., Horton J.D., Identification of a Mammalian Long Chain Fatty Acyl Elongase Regulated by Sterol Regulatory Element-binding Proteins."; J. Biol. Chem. 276:45358-45366 [2001].
                                               17;
               Length 316;
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Nagarajan R., Le N.H., Mahoney H., Araki T., Milbrandt J.D.,
"Deciphering Peripheral Nerve Myelination Using Schwann Cell
Expression Profiling.",
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                               Indels
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            31.4%; Score 484.5; DB 5; 37.7%; Pred. No. 7.9e-35; ive 54; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                 254 NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
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STRAIN=CZECH II, TISSUE=Breast tumor;
                                              Conservative
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                              Similarity
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                                            103;
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            Query Match
Best Local S
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 SAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVT 264
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                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                       STRAIN=Sprague Dawley; TISSUE=Liver;

A Inagaki K., Aki T., Fukuda Y., Kawamoto S., Shigeta S., Ono K.,

A Inagaki K., Aki T., Fukuda Y., Kawamoto S., Shigeta S., Ono K.,

A unagaki K., Aki T., Fukuda Y., Kawamoto S., Shigeta S., Ono K.,

B Inagaki K., Aki T., Fukuda Y., Kawamoto S., Shigeta S., Ono K.,

I "Identification and expression of a mammalian fatty acid elongase involved in de novo biosynchesis of C18 fatty acids.";

I mvolved in de novo biosynchesis of C18 fatty acid elongase involved in de novo biosynchesis of C18 fatty acid elongase.

I mvolved in de novo biosynchesis of C18 fatty acid elongase involved in proposition to the EMBL/GenBank/DDBJ databases.

R CO: G0:0016021; C:integral to membrane; IEA.

RO: G0:0016021; C:integral to membrane; IEA.

R InterPro: IPRO20206; ONSI_SUR4.

R Pfam: PF01151; ELO: 1.

R PROSITE; PS01168; ELO: 1.

R PROSITE; PS01168; ELO: 1.
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01-XAR-2003 (TrEMBLrel. 23, Last sequence update)
01-XAR-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ELOYL6 Chair farty acyl elongase.
ELOYL6 Chair (Mouse).
Mus musculus (Mouse).
Bukaryora; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryora; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.
NCBF_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              28.9%; Score 446.5; DB 11; Length 267; 36.9%; Pred. No. 1.5e-31;
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                           232 DNIVWASLMYLSYLLLFSSFFYQSYM--KSSKPESIKRE 268
           253 ANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSVKKE 291
                                                                                                                                           Last sequence update)
Last annotation update}
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                                                                                                                               Created)
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YLLLPCHFFFEAYIGKVKKATKA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                    PRELIMINARY;
                                                                                                                                                                     Fatty acid elongase 2
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                                                                        RESULT 5
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Skin;

TABLINE=C3734683; PubMed=12466851;

The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A thalysis of the mouse transcriptome based on functional annotation of an of 770 full-length cDNAs.";

Nature 420:563-573(2002).

R MGD; MGI:2156528; Elov16.

DR MGD; MGI:2156528; Elov16.

DR GO; GO:0016747; F:transferase activity, transferring groups o. .; IDA.

DR GO; GO:003497; P:fatty acid elongation; IDA.

DR HerPro; IPRO02076; GNS1_SUR4.

Pfam; PF01151; ELO; 1.

SRQUENCE 267 AA; 31601 MM; 4031P9C503E4DD23 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 RAAGFRUSRKFAMFITLSQITÇMLMGCVINYLVFNWMQHDNDQCYSHFQNIFWSSLMYLS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 LGDTMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 SAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPÇQQSVANLYLAFVIYVT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 ILWNGALAAFSIIATLRFSIDPLRSLYAEGPYKTLC-YSCNPTDVAAFWSFAFALSKIVE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 SYEPEKQFNENEAIQ---W---MOENWKKSPLFSALYAAFIFGGRHLMNKRAKFELRKPL 63
                                                                                                                                                                                                                                                                                                                                                                                 .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 KYKYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto & Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogano S., Sugano S., Submit cDNA sequencing project.", Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
28.4%; Score 439.5; DB 11; Length
Best Local Similarity 36.5%; Pred. No. 6.3e-31;
Matches 96; Conservative 50; Mismatches 110; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO27031; BAB15632.1; -.
Genew; HGNC:15829; ELOVL6.
GO: GO:0016021; C:integral to membrane; IEA.
Interpro; IPRO02076; GNS1_SUR4.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein FLJ23378.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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셤 ò P P ò 셤 ò g ò

us-09-936-845a-15.rspt

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226 QMLAGVGITWMVYKVKTEYKLÞCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKS 285
                              180 QMLMGCVVNYLVFCWMQHDQ--CHSHPQNIFWSSLMYLSYLVLFCHFFFEAYIGKMRKTT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 GFVASYCQNENYYTDASTGFWGWAFVWSKAPBLGDTWFLVLRKKKPVIFWHHHALTFVY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 TVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 ITWWYKVKTEYKLP-CQOSVANLYLAFVIYYTFAILFIQFFVKAYIIKSSKKSKKVKB 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 IFGHLVFIKSADSVPGCAVSMNVLSIGGLMYISYLPLFAKFFYKAVIQKRS-PTKTSKQE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 SITISVLYPILIKVIQKFMENRKPPTLKYPLILMNGALAAPSIIATLRFSIDPLRSLYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 GPYKTLCYSCN-PTDVA-AFWSFAPALSKIVELGDTMFIILRKRPLIFLHYYHHAAVLIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 AVVTYSEHQAWARWSLALMLAVHTVMYFYFAVRALMIQTPRPVAKFITTIQIVQFVISCY
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.8%; Score 398; DB 5; Length 27 larity 37.1%; Pred. No. 3e-27; Conservative 48; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
BMBL; 281058; CAB02921.1; -.
PIN; 120706; T20708.
WormPep; F11E6.5; CE19785.
GO; GO: GO16021; C: integral to membrane; IEA.
InterPro; IFRO02076; GNS1_SUR4.
PEam; PF01151; ELO; GNS1_SUR4.
SEQUENCE 274 AA; 31361 MW; 2CBB7DASF418D714 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cryptosporidium parvum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UJV-2003 (TrEMBLrel. 24, Last annotation update)
011B6.5 protein.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Putative fatty-acyl elongase.
                                                                                                                                                                                                                        274 AA
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                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
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Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                    |:
238 KA 239
                                                                                  286 KS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matthews
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                                                                                                                                                                                                                                                                                     203 TVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMYYKVKTBYKLPCQQSVANLYLAFVIY 262
                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                      64 VLWSLTLAVFSIFGALRIGAYMVYILMTKGLKÇSVCDQGFYNGP--VSKFWAYAFVLSKA 121
                                                                                                                                                                                                                                                                                                                                                                                            62 YILMTKGLKQSVCDQGFYNGP--VSKFWAYAFVLSKAPELGDTIFIILRKQKLIFLHWYH 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Suzuki Y., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., A Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., A Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Aotsuka S., Nagahari K., A Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Nagahari K., A Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Sasaki N., Thibo human cDNA sequencing project.", "NEDO human cDNA sequencing project.", Submitted (MAR-2002) to the BMBL/GenBank/DDBJ databases.

R EMBL, AKO74813; BAC11225.1; -. MEMBL/GenBank/DDBJ databases.

R EMBL, EMBL, ELO, I. cintegral to membrane; IEA.

R InterPro; IPR002076; GNS1_SUR4.

R Pfam; PF01151; BLO; 1.

R PROSITE; PS01188; ELO; 1.

R HYDOChetical protein.

R HYDOChetical protein.
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                                                                                                                                                            :|::
EYEFEKQFNENBAIQ---W---MGENWKKSFLFSALYAAFIFGGRHIMNKAKFELRKPL
                                                                                                                                                                                                               86 ILWNGALAAFSITATLRFSIDPLRSLYAEGFYKTLC---YSCNPTDVAAFWSFAFALSKI
                                                                                                                                 26 KYKYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QENWKKSFLFSALYAAFIFGGRHLMNKRAKFELRKPLVL#SLTLAVFSIFGALRTGAYMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 QKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                13;
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                                                           DB 4; Length 265;
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                                                     / Match 28.2%; Score 435.5; DB 4; Length:
Local Similarity 35.8%; Pred. No. 1.4e-30;
Nes 95; Conservative 54; Mismatches 103; Indels
  l protein.
265 AA; 31376 MW; 01234E0EEF6CE341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FL390332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                263 VTFAILFIQFFVKAYIIKSSKKSKS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 LSYLVLFCHFFEAYIGKMRKTTKA 264
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nes 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homeo sapiens (Human).
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Hypothetical
SEQUENCE 26
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                            Matches
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9

q ò g ò 9

Gaps

20;

Length 274;

DDF0840C1454A4CD CRC64;

membrane; IEA

140

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60 TGPLNLANAGLAIFSTLGSLATTFGLLHEFFSRGFFESYHHIGDFYNGLSGMFTWLFVLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 KVAEPGDILFIIILRKKPLMFLHWYHHVLTMNYAFMSFEANLGFNTWITWMNFSVHSIMYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYTVSAMGYRLPKAVSMTVTTVQTTQMLAGVGJTWMVYKVKTEYKLPCQQSVAN----LY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 KYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLCYSCN-PTDVAAFWSFAFALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 KIVELGDIMPIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYT
                                                                                                                                                                                                                                                                                                    22 DMTTKYKYSYHPPGBQVADPQYWTILPQKYWYHSITISVLYFILIKVIQKFMENRKPFTL
                                                                                                                                                                                                       Query Match

24.2%; Score 374; DB 5; Length 27.

Best Local Similarity 30.4%; Pred. No. 4e-25;

Matches 83; Conservative 59; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 PCLLMBISYVVLFGNFYYQSYIKGGGKKFNAEK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 LAFVIYVTFAILFIQFFVKAYIIKSSKKSKKVK 289
EMBL; U61954; AAK29807.1; -.
PIR; H88690.
MormPepp; P41H10.8; CE10286.
GO; GO:0016021; C:integral to me InterPc; IPR002076; GNS1_SUR4.
PROSITE; PR01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
SEQUENCE 274 AA; 31671 NW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 NIFLALFSFIGTLALMPYVLTNITKYGFVSSI----CSPPIAPLTKGPAGLWLSLFIYSKY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 TVSAMGYRLPKHVSMTVTTVQTTQMLAGVGIT--WMVYKVK-----TÄY----KLP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 YLSSCGKR-PKW-GMIITILQIVQMIIGTILTTSGMYYSYKHPFANVFPVBYLSQPLKVG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 QYWTILPQXYW-----YHSITISVLYFILIKVIQKFMENRKPFTLKYPLILM
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                   STRAIN=IOWA;
Millership J.J., Zhu G.;
"Putative long-chain fatty-acyl elongase gene from Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                         39;
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                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 323;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
25.7%; Score 396.5; DB 5; Length 3;
Best Local Similarity 36.4%; Pred. No. 4.8e-27;
Matches 100; Conservative 35; Mismatches 101; Indels
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Blanchard M., Bacdshaw H.;
"The sequence of C. elegans cosmid F41H10.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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STRAIM=Bristol N2;
STRAIM=Bristol N2;
SUBMITTED (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                          parvum.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                               EMED.; AY204875; AA034582.1; -. GO; GO:0016021; C:integral to membrane; IEA. InterPro; IPR002076; GNS1_SUR4.
Pfam: PF01151; ELO; 1. SPRGSTIE; ELO; 1. SEGUIENCE 323 AA; 38325 MW; 8AF64F586F9B1ED0 CRC64;
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Last sequence update |
Last annotation update |
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    Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                              Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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23.8%; Score 368; DB 5; Length 301;
Best Local Similarity 33.5%; Pred. No. 1.5e-24;
Matches 84; Conservative 52; Mismatches 103; Indels 12;
                                                                                                                                                                                                                                                                                                                                 Quail
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A physical map of the Leishmania major Friedlin genome."; Genome Res 8:135-145(1998).

EMBL; AL499614; CAC10865.11; --

EMBL; AL499614; Cacinesaral to membrane; IEA.

InterPro; IPR022076; GNS1_SUR4.

PROSTTE; PS01151; BLO; 1.

PROSTTE; PS01188; ELO; 1.

SEQUENCE 301 AA; 34215 MW; P610DDDA156B1549 CRC64;
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                                                                         Last sequence update)
301 AA
                                                 Created)
  PRT;
                                              (TrBMBLrel. 16, C
(TrBMBLrel. 16, I
(TrBMBLrel. 24, I
  PRELIMINARY;
                                                                                                                                Transmembrane protein
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203 IVSAMGYRLPKNVSWTVTTVQTTQMLAGV-GITWMVYKVKT-SYKLPCQQSVANLYLAFV 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SLWSLLTNQDEVFPHIRARRFIQEHFGLFVQMAIAYVILVFSIKRFWRDREFFQLITALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 IMMGALAAFSIIAT---LRFSIDPLRSLYAEGFYKTLCYS-CNPTDVAAFWSPAFALSKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Science 282:2012-2018 (1998).
EMBL; 267493. CA592960.1; -.
PIR; T22791; T22791.
Wormbep; P56411.3; CE116144.
GO; GO:0016621; C:integral to membrane; IEA.
InterPro; IPR002076; GNS1_SUR4.
PROSTIE; P801188; ELO; 1.
SEQUENCE 281 AA; 33141 MW; 825D529D7FEBF936 CRC64;
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Last annotation update)
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31.7%; Pred. No. 3.9e-21;
iive 49; Mismatches 93;
                                                                                                                                                                                                                                              281 AA.
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MEDLINE=99069613; PubMed=9851916;
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Q203100 (CASMELRE) 01, C.
01-NOV-1996 (TEMBLEE) 01, L.
01-NOV-1996 (TEMBLEE) 01, L.
01-MOV-2003 (TEMBLEE). 24, L.
F41H10.7 protein.
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24,
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nes 77; Conservative 4
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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Caenorhabditis elegans.
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                          286 KSV
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                                                           161
                                                                                                                                                                                  HYYHHAAVLIYTVHSGABHTAAGRFYILMNYFAHSLMYTYYTVSAMGYR-LPKWVSMTVT 220
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28 FDDYFDVLVYSEVLYVLIVPLGPKAMESREPYRLRYLIAAWNLALSFLSLCGTIGVSIML 87
                                                                                            40 FADHFDVTIQASILYMVVVEGTKWEMRNRQPFQLTIPINIWNFILAAFSIAGAVKMTPEF
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Rhabditidae, Peloderinae, Caenorhabditis.
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31.3%; Pred. No. 7.2e-24;
ive 58; Mismatches 107; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amoration update)
Long chain_POLYUNSATURATED fatty acid elongation enzyme.
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IPR002076; GNS1_SUR4.

Pfam; PF01151; ELO; 1.

PROSTTR; PS01188; ELO; 1.

SEQUENCE 288 AA; 33561 MW; 8BA5CD4892012B0E CRC64;
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EMBL; Z68749; CAA92958.1; -.
PIR; T22789; T22789.
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CEELO1 OR F56H11.
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D2 C2090
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Caenorhabditis elegans

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 AGV-GITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKS 287
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      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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21.2%; Score 327.5; DB 5; Length 286;
Best Local Similarity 32.8%; Pred. No. 5.4e-21;
Matches 80; Conservative 44; Mismatches 109; Indels 11.
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SEQUENCE FROM N.A.
STRAIN-Briscol N2;
Waterston R;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U61954; AAK29808.1; -.
FIR; E88690; E88690; E86690; E86690; E86600; CEL0284.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro.; PRO12076; GNSI_SUR4.
Pfam; PP01151; ELO; 1.
SEQUENCE 286 AA; 33102 MW; C50E1180DCB10AC3 CRC64;
                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Blanchard M., Bradshaw H.;
Blanchard M., Bradshaw H.;
submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
STRALINEBTISCO1 N2;
MEDLINE=99069613; PubMed=9851916;
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274 AKDQ 277
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35, Appl 45, Appl 2, Appl 2, Appl 16, Appl 16, Appl 165, Appl 85, Appl 21, Appl 21, Appl 25, Appl 26, Appl 26, Appl 27, Appl 28, Appl 28, Appl 28, Appl

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HSIMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGI-TWMVYKVKTEYKLPCQQSVA 253
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Best Local Similarity 37.7%; Pred. No. 3.3e-44;
Matches 103; Conservative 54; Mismatches 99; Indels 17
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CTHER INFORMATION: Xaa = Unknown or Other at position 235
US-09-903-456-58
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APPLICANT: MAKETJi, Pradip
APPLICANT: MAKETJi, Pradip
APPLICANT: MAKETJi, Pradip
APPLICANT: MAKETJi, Pradip
APPLICANT: Haeng, Yung-Sheng
APPLICANT: Heenard, ELONGASE GENES AND USES THEREOF
ITILE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFRENCE: 6407.US.P3
CURRENT RILING DATE: 2001-07-11
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FESTERE OF Windows Version 4.0
SEQUENCE: ABSTERED OF WINDOWS OF SEQUENCES OF TAXABLE O
US-09-903-456-78
US-09-903-456-79
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US-09-903-456-83
US-09-903-456-83
US-09-903-456-61
US-09-903-456-61
US-09-145-828-16
US-09-903-456-68
US-09-903-456-68
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US-09-903-456-58
; Sequence 58, Application US/09903456
netent No. 6677445
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ORGANISM: Drosophila melanogaster
      NAME/KBY: VARIANT
      195
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24, Appl
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66, Appl
55, Appl
111, Appl
112, Appl
115, Appl
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1 MELAZFWNDLNTFTIYGPNH......FFVKAYIIKSSKKSKVKNE 291
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Sequence 1
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Sequence 4
Sequence 7
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Sequence 8
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/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-903-456-53

US-09-903-456-24

US-09-903-456-64

US-09-903-456-64

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US-09-145-828A-13

US-09-145-828A-13

US-09-145-828A-13

US-09-145-828A-18

US-09-903-456-15

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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228 LAGV--GITWMVYKVKTBYKLPCQQSVANLYLAFVIYVTFALLFIQPFVKAYIIKSSK-K 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 RSLYABGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTWFIILRKRPLIFLHYYHHA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 BEYWVSSFLIVVVVYLLLIVVGQTYMRTRKSFSLQRPLILMSFFLAIFSILGTLRMWKFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQM
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
31.0%; Score 479; DB 4; Length 27
Best Local Similarity 41.6%; Pred. No. 1.6e-43;
Matches 101; Conservative 47; Mismatches 87; Indels
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; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-09-903-456-24
                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: VARIANT
LOCATION: (272)...(272)
OTHER INFORMATION: Xaa = Unknown or other at position 272
US-09-145-828A-18
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APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Mukerji, Pradip
APPLICANT: Heang, Yung-Sheng
APPLICANT: Heang, Yung-Sheng
APPLICANT: Bereira, Sizette L.
TITLE OF INVENTION: BLONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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FILE REFERENCE: 6407.US.O1
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-69-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 272
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NAME/KEY: VARIANT
LOCATION: (272)...
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                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 TVLLPTSFGYKNKVPSGGWFWTWNFGVHSVMYTYYTMKAAKLKHPNLLPWVITSLQILQM 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTMFILLRKRPLIFILHYYHHA 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 TVMFTVGLKQTVCPAIYTDDAVVRFWSFLFLSKVVELGDTAFILLRKRPLIFVHWYHHS 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 271;
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Patent No. 6403349
Patent No. 6403349
APPLICANT: Mukerji, Pradip
APPLICANT: Laonard, Amanda E. Y.
APPLICANT: Thurmond, Janada E. Y.
APPLICANT: Thurmond, Jennifer
APPLICANT: Archner, Stephen J.
APPLICANT: Archner, Stephen J.
APPLICANT: Archner, Stephen J.
APPLICANT: Thurmond, Jennifer
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APPLICANT: Leonard, Amanda Bun-Yeong

APPLICANT: Leonard, Amanda Bun-Yeong

APPLICANT: Hensy, Yung-Sheng

APPLICANT: Hensy, Yung-Sheng

APPLICANT: Bereira, Suzette L.

TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF

FILE REPREMENT: 6407.08. P3

CURRENT APPLICATION NUMBER: US 09/624,670

PRIOR APPLICATION NUMBER: US 09/379,095

PRIOR APPLICATION NUMBER: US 09/379,095

PRIOR FILING DATE: 1999-08-23

PRIOR FILING DATE: 1999-08-23

PRIOR FILING DATE: 1999-08-23

PRIOR FILING DATE: 1998-08-23

PRIOR FILING DATE: 1998-08-23

PRIOR FILING DATE: 1998-08-5

SEQ ID NO 53

LENGTH: 271
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                                                                                                         ; Sequence 53, Application US/09903456; Patent No. 6677145
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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Best Local S
Matches 101
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DB 4; Length 265;
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Laboratories
APPLICANT: Laboratories
APPLICANT: Laboratories
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVERTION: ELONGASE GENES AND USES THEREOF
FILE REPRENCE: 607.405.P3
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR PLICATION NUMBER: US 09/624,670
PRIOR PLILING DATE: 1999-08-23
PRIOR PLILING DATE: 1999-08-23
PRIOR PLILING DATE: 1999-08-23
PRIOR PLILING DATE: 1999-08-23
PRIOR PLILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 64
SEQ ID NOS: 116
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APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Leonard, Vung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: BLONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.2%; Score 435.5; DB 4;
35.8%; Pred. No. 7.5e-39;
tive 54; Mismatches 103;
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US-09-903-456-55
US-09-903-456-55
Sequence 55, Application US/09903456
Patent No. 6677145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  5-09-903-456-64
Sequence 64, Application US/09903456
Patent No. 6677145
GENERAL INFORMATION:
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Best Local Similarity 35.8'
Matches 95; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                             281 SSKKSK 286
                                                                                                                                                                               253 GGHKSR 258
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                                                                                                                                                                                                                                                    : | | | ::: :::| | | ::: :::| | :::| | ::| | ::| | ::| | ::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | ::
                                                                                                                 49 QKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPE 108
                                                                                                                                                                                                                                                                                                                                                                                           AVLIYTVHSGAEHTAAGRPYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQW 227
                                                                                                                                                                                                                                                                                                                                                                                                                               228 LAGV--GITWMVYKVKTEYKLPCQQSVANEYLAFVIYVTFALLFIQFFVKAYIIKSSK-K 284
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                                                                                                                                                         32 EEYWVSSFLIVVVYLLLIVVQQTYMRTRKSFSLQRPLILMSFFLAIFSILGTLRNWKFMA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 WIWVE---YYCGI-----YMLVIFGGQHFMQNRPRPQLRGPLIIWNTLLAMFSIMGAART
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40.2%; Pred. No. 2.8e-43;
tive 49; Mismatches 87; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAMEN/KEY: VARIANT
LOCATION: (218)...(218)
OTHER INFORMATION: Xaa = Unknown or Other at position 218
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APPLICANT: Mukerii, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPRESENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 201-07-11.
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 116
          Best Local Similarity 41.6%; Pred. No. 1.6e-43; Matches 101; Conservative 47; Mismatches 87;
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Patent No. 6677145
GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
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Matches 99; Conservative
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LENGTH: 261
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86 ILWNGALAAPSIIATLRFSIDPLRSLYAEGFYKTLC---YSCNPTDVAAFWSFAFALSKI 142
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                                                                                                                                                                                                                                  143 VELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYY 202
                                                                                                                                                                                                                                                                                                                                                      203 TVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIY 262
                                  10 BYBFEKÇİNENBAIQ---#--MQENWKKSPLFSALYAAFIFGGRHLMYKRAKFELRKDI. 63
                                                                                                                                                                                                                                                                       26 KYKYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL
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48 FQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                          167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226
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                                         17 FADHEDVIQASILYMVVVEGTKWENRURQPPQLTIPLNIMNFILAAFSIAGAVKMTPEF 76
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APPLICANT: Honard, Amanda Bun-Yeong
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Bereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPERENCE: 640.108. P.3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 1999-08-33
PRIOR PILING DATE: 1999-08-33
PRIOR APPLICATION NUMBER: US 09/145,828
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US-09-903-456-56
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257 KAV 259
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Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Laboratories
APPLICANT: Lenard, Manda Bun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette I.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPERENCE: 607.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-09-12
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FREICE FREICE (FOR WINDOWS VERSION 4.0)
SEQ ID NOS: 116
                                      CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION WHRER: US 09/624,670
FRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1998-09-02
NUMBER: OF SEQ ID NOS: 116
SEQ ID NO 55
           CURRENT APPLICATION NUMBER: US/09/903,456
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Patent No. 6677145
GENERAL INFORMATION:
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US-09-903-456-89
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nes 76; Conserv
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US-09-903-456-55
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match. 23.3%; Score 360; DB 4; Length 288; Best Local Similarity 31.3%; Pred. No. 1.1e-30; Matches 76; Conservative 58; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEREOF
                                                                APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Heanay, Yung-Sheng
APPLICANT: Heanay, Yung-Sheng
APPLICANT: Bereira, Suzette L.
ITILE OF INVENTION: BLONGASE GENES AND USES THEREOF
FILE REFRENCE: 6407 US. P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2001-07-11
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Thurmond, Jennifer
APPLICANT: Airchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
TILLE OF INVENTION: THE BLONGASE GENE AND USE,
TILLE REFERENCE: 8407-108.01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
MUNDBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Wi-'.
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Sequence 62, Application US/09903456 Patent No. 6677145 GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Caenorhabditis elegans US-09-903-456-62
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US-09-145-828A-13
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                                                                                                                                                                                                                                                                             79
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                                                                                                                                                                                                                             49 OKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL1LWNGALAAFSIIAT---LRFSI
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Lourard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Shang
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELLOWGASE GENES AND USES THEREOF
FILE REPERENCE: 607.US.P3
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SURVARE: FastSEQ for Windows Version 4.0
LENGTH: 238
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                                                                                                                          Query Match 21.2%; Score 327.5; DB 4;
Best Local Similarity 33.9%; Pred. No. 2.8e-27;
Matches 75; Conservative 46; Mismatches 91;
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33.9%; Pred. No. 2.8e-27;
tive 46; Mismatches 91
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LENGTH: 238
TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Caenorhabditis elegans
US-09-903-456-20
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Best Local Similarity 33.9'
Matches 75; Conservative
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                                                                                      APPLICANT: Abboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda B. Y.
APPLICANT: Leonard, Amanda B. Y.
APPLICANT: Leonard, Amanda B. Y.
APPLICANT: Thurmond, Jennifer
APPLICANT: Thurmond, Jennifer
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
APPLICANT: FIRCHNER, Stephen J.
APPLICANT: FIRCHNER, Stephen J.
APPLICANT: FIRCHNER, Stephen J.
APPLICANT: PARKENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09903456
Patent No. 667745
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Honory Amenda Bun-Yeong
APPLICANT: Honory Yung-Sheng
APPLICANT: Honory Yung-Sheng
APPLICANT: Honory Yung-Sheng
APPLICANT: Honory Yung-Sheng
APPLICANT: Perelra, Suzette L.
TILLE OF INVENTION: ELDOGASE GENES AND USES THEREOF
FILLE REPRENCE: 6407.US. P3
CURRENT APPLICATION NUMBER: US 09/624,670
FRICR APPLICATION NUMBER: US 09/379,095
FRICR FILING DATE: 2000-07-24
FRICR APPLICATION NUMBER: US 09/379,095
FRICR FILING DATE: 1999-08-23
FRICR FILING DATE: 1999-08-23
FRICR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
                    Sequence 11, Application US/09145828A
Patent No. 6403349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11
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US-09-145-828A-11
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US-09-903-456-18
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LENGTH: 278
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89 DGFSHTYSHVSELYIDSTSGYMIFLWVISKIPELDIVFIVLRKRPLIFMEMYHHALIGY 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 AGV-GITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTPAILFIQFFVKAYIIKSSKKSKS 287
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                                                                                                                                                                  Query Match
21.2%; Score 327.5; DB 4; Length 2
Best Local Similarity 32.8%; Pred. No. 3.5e-27;
Matches 80; Conservative 44; Mismatches 109; Indels
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LOCATION: (141)...(141)
OTHER INFORMATION: Xaa = Unknown or Other at position 141
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APPLICANT: Mikerji, Pradip
APPLICANT: Mikerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
TITLE OF INVEXTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 116
SOCTWARRS: FastSEQ for Windows Version 4.0
SEQ ID NO 4.0
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; Sequence 47, Application US/09903456
; Patent No. 6677145
; SEQ ID NO 18

: LENGTH: 278

: TYPE: PRT

: ORCAMN:SM: Caenorhabditis elegans

US-09-903-456-18
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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61 AGFRVSRKFAMFITLSQITQMLMGCVVNYLVFCWMQHDQ--CHSHFQNIFWSSLMYLSYL 118

q දු දු

267 ILFIQFFVKAYIIKSSKKSKS 287 :|| || || || || || || 1 119 VLFCHFFFFAYIGKMRKTTKA 139

Search completed: June 16, 2004, 15:30:08 Job time : 24 secs